

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 17:00:29 ; Search time 2253.73 Seconds
(without alignments)
1983.487 Million cell updates/sec

Title: US-09-698-903B-10

Perfect score: 416

Sequence: 1 ctacggcaatgtaccagctg.....catgaacacccaaactcgat 416

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estfun: *
2: em_esthum: *
3: em_estin: *
4: em_estom: *
5: em_estpl: *
6: em_estba: *
7: em_estro: *
8: em_estov: *
9: em_hic: *
10: gb_est1: *
11: gb_est2: *
12: gb_hic: *
13: gb_gss: *
14: em_gss_fun: *
15: em_gss_hum: *
16: em_gss_inv: *
17: em_gss_pln: *
18: em_gss_pro: *
19: em_gss_rod: *
20: em_gss_vrt: *
21: em_gss_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	63.2	15.2	734	13	CNS010MP
C 2	58.8	14.1	1101	13	CNS00238
C 3	56.6	13.6	1101	13	CNS0042W
C 4	55.8	13.4	537	13	AQ506817
C 5	55.6	13.4	421	13	AQ917446
C 6	55.4	13.3	300	13	AQ098895
C 7	55.2	13.3	844	13	CNS03D0I
C 8	55.2	13.3	845	13	AQ745337
C 9	55.2	13.3	1101	13	CNS00K47
C 10	55	13.2	980	13	CNS00JG1
C 11	54.8	13.2	928	13	CNS00DKY
C 12	54.8	13.2	980	13	CNS00JG1

13	54.6	13.1	1101	13	CNS00EVL
14	54.4	13.1	678	13	CNS02AOC
15	53.8	12.9	1337	5	BF630719
C 16	53.6	12.9	1101	13	CNS003BA
C 17	53.2	12.8	340	10	AL514737
C 18	53.2	12.8	1101	13	CNS003BB
19	53.2	12.8	1203	13	CNS015WU
20	53	12.7	421	13	AQ917446
21	53	12.7	1101	13	CNS00EYK
22	53	12.7	1169	13	CNS06KHQ
C 23	52.8	12.7	725	13	AQ917102
C 24	52.8	12.7	1141	13	CNS07206
C 25	52.6	12.6	1101	13	CNS00EO7
C 26	52.6	12.6	1101	13	CNS00EVL
C 27	52.4	12.6	697	13	CNS04707
28	52.4	12.6	725	13	AQ917102
29	52.4	12.6	1101	13	CNS001FB
30	52.2	12.5	458	10	AU086681
C 31	52.2	12.5	500	10	AU086078
C 32	52.2	12.5	1101	13	CNS00BO1
C 33	52.2	12.5	1101	13	CNS0161I
C 34	51.8	12.5	1101	13	CNS00FMC
C 35	51.6	12.4	377	13	AQ012444
C 36	51.6	12.4	711	13	AQ051188
C 37	51.4	12.4	1101	13	CNS0039G
C 38	51.4	12.4	1225	13	CNS0161D
C 39	51.2	12.3	517	13	AZ929020
C 40	51.2	12.3	1085	13	CNS02PW4
C 41	51	12.3	340	10	AL514737
C 42	51	12.3	764	13	AQ915359
C 43	51	12.3	1101	13	CNS0161I
C 44	50.8	12.2	500	10	AU086152
C 45	50.6	12.2	901	13	AZ551119

ALIGNMENTS

RESULT 1
CNS010MP/c

LOCUS
DEFINITION

CNS010MP 734 bp DNA GSS
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04L20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL099163 GI:5610774

VERSION

AL099163.1

KEYWORDS

GSS.

SOURCE

fruit fly.

ORGANISM

Plasmid Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 734)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ;

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pheloBAC11.

FEATURES

source

Location/Qualifiers

1..734

/organism="Drosophila melanogaster"

/plasmid="pBelobAC11"

/db_xref="taxon:7227"

/clone_lib="DrosBAC"

/clone="BACN04L20"


```

Db 815 TATATATAAGAAVAATATATTAATWAAATANTATANTATATATATTTAAATTTATTCA 874
Qy 200 taattataataattataactgaacaccggtgccccctgctgctttacatgga 259
Db 875 TWAATAATAATTTTAAATATTAATWAAATAAATAATWTTTAAATATATATTTTAAATTT 934
Qy 260 ttctcgcgtactattgtatatacgtatataatccgtata-atgacatatatttat 318
Db 935 TKTTATTTTAMDATWTTTATTTATATATWTAATAAAATWTAATAAAATWTAATAATATAT 994
Qy 319 gaacataatacgtctgagtggtcttcacgcgtgaagagtttcaatatgtaagtga 378
Db 995 WTAAATAAAATWTTTATTTTGTAAATAATWTAATAAAATWTTTAAATATATATATA 1054
Qy 379 agagtcacaaaccccaatcatgaa 402
Db 1055 AAKTTTAAATWAAATWAAAW 1078

RESULT 4
AQ506817 537 bp DNA GSS 29-APR-1999
LOCUS RPCI-11-281J17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-281J17
DEFINITION , DNA sequence.
ACCESSION AQ506817
VERSION AQ506817.1 GI:4711564
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 537)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RPCI-11-281J17.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: bheetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.
Seq primer: T7
Class: BAC ends.
FEATURES
source
1. .537
/organism="Homo sapiens"
/db_xref="GDB:7607752"
/db_xref="taxon:9606"
/clone="RPCI-11-281J17"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC library"
BASE COUNT 216 a 11 c 30 g 280 t
ORIGIN

Query Match 13.4%; Score 55.8; DB 13; Length 537;
Best Local Similarity 48.5%; Pred. No. 0.21;
Matches 150; Conservative 1; Mismatches 158; Indels 0; Gaps 0;

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Qy 21 atataacagttattgaataatttctgaatttaaacctgcatcaataaawttatgttttt 80
Db 99 ATATATGATATATATGATATATATTTATATATATATATATATATATATATATATATAT 158
Qy 81 gctggactataacacctgacctgtttattttatcaataaattttaaacatataattcttt 140
Db 159 TTATATATATGATATATATATTTATATATATATATATATATATATATATATATATTT 218
Qy 141 caagatgggaattaaacatctcaaaattgcctttcttctatcgaccatgacatccctacc 200
Db 219 ATATATGATATATATATTTATATATATTTGATATATATATGATATATATATATATAT 278
Qy 201 aattataaattataattataactgaacaccatgggtgccccctgctctttacatggat 260
Db 279 ATATTTATATATTTATATATATATATATATATATATATATATATATATATATATATAT 338
Qy 261 ttctccgctactattgtatatacgtgatatataacgtataaagtacatatatttatatga 320
Db 339 GTATATATTTATATATATATTTATATATATATATATATATATATATATATATATAT 398
Qy 321 acatgatta 329
Db 399 ATATATTTTA 407

RESULT 5
AQ917446/c 421 bp DNA GSS 07-DEC-1999
LOCUS T233481b Medicago truncatula BAC library Medicago truncatula
DEFINITION genomic clone 15E22, DNA sequence.
ACCESSION AQ917446
VERSION AQ917446.1 GI:6537021
KEYWORDS GSS.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 421)
AUTHORS Kim,D., Limpens,E., Peng,H., Ellis,L. and Cook,D.R.
TITLE BAC end sequencing of Medicago truncatula
JOURNAL Unpublished (1999)
COMMENT Contact: Cook DR
The Crop Biotechnology Center
Texas A&M University
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Peterson Bldg, College Station, TX 77843-2132, USA
Tel: 409 845 8743
Fax: 409 862 4790
Email: dcook@ppserver.tamu.edu
Other name: DK457-L; date: 8/12/99; Submitted to the Database of
Genome Survey Sequences (GSS) on 12/06/99; More information is
available at 'http://chrystie.tamu.edu/medicago'.
Seq primer: SQ-BAC-L (AACGCCAGGGTTTCCCGAGTCACGACG)
Class: BAC ends.
FEATURES
source
1. 421
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="15E22"
/clone_lib="Medicago truncatula BAC library"
/notes="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII; Nam. Y-W, Penmetza, R.V., Endre, G., Kim, D., and
Cook, D.R. 1999. Construction of a bacterial artificial
chromosome library of Medicago truncatula and
identification of clones containing ethylene response
genes. Theor Appl Genet 98: 638-646."
BASE COUNT 191 a 19 c 5 g 205 t
ORIGIN

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```

Query Match      13.4%; Score 55.6; DB 13; Length 421;
Best Local Similarity 48.1%; Pred. No. 0.24;
Matches 154; Conservative 1; Mismatches 165; Indels 0; Gaps 0;

QY 21 atatacagctattggaattcttgaattttaaacttgcatcaataaaawttatgttttt 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 gcttggaactaatacactgactgtgttttttcaataaataattttaaactatattcttt 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 141 caagatgggaataacacatcaccaattgaccttcttccgacctgacacacctaccat 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 201 aattaaataataataataactgaaacacatggtgccccctgctgctttacacatgat 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 261 ttctccgctactattgtatcactgtatataccgataatgacatatattttatga 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 CACTCTATATATATATATATATATATATATATATATATATATATATATATATATAT 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 321 acatgatgaatgctgtgag 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 ATATATATATAGAGAGAG 43
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
ACQ098895.6
LOCUS      HS_3050_A1_C03_MR_C1T Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate-3050 Col-5 Row=E, DNA sequence.
ACCESSION  AQ098895
VERSION     AQ098895
KEYWORDS    AQ098895.1 GI:3469924
SOURCE      GSS.
ORGANISM    human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 300)
AUTHORS     Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE       Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL     Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE     99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallaceu.washington.edu
            Sequence Tagged Connector
            Plate: 3050 row: E column: 5
            Class: BAC ends
            High quality sequence stop: 300.
            Location/Qualifiers
            1..300
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="Plate-3050 Col-5 Row=E"
            /clone_lib="CIT Approved Human Genomic Sperm Library D"
            /sex="male"
            /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
            E-Coli DH10B"

BASE COUNT  150 a      8 c      4 g      138 t
ORIGIN

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Query Match      13.3%; Score 55.4; DB 13; Length 300;
Best Local Similarity 49.5%; Pred. No. 0.28;
Matches 140; Conservative 1; Mismatches 142; Indels 0; Gaps 0;

QY 33 attgaatatattctgaattttaaacttgcatcaataaaawttatgtttttgctggactata 92
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAA 75
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 93 atacctgactgtttatttcatcaataaataatttcaaactatatttcttccaagatggaaat 152
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 153 taacatctacaaattgaccttcttcttccgacctgacacacctaccacataattatatt 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 136 AATCTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 213 aattataataactgaaacacatggtgccccctgctgctttacacatggatttctccgctact 272
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 273 atttgtacgtgtatataccgtataatgacatatatttta 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 ATATATCTATGATATAATATATATATATATATATATATATATATATATATATATA 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
CNS03D01
LOCUS      844 bp DNA GSS 15-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
            015L14 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL238491
VERSION     AL238491.1 GI:7897626
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
ORGANISM    Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
            1 (bases 1 to 844)
REFERENCE   1
AUTHORS     Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
TITLE       Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 844)
AUTHORS     Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE       Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
JOURNAL     Unpublished
REFERENCE   3 (bases 1 to 844)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (12-APR-2000) to the EMBL/GenBank/DDJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
            Location/Qualifiers
            1..844
            /organism="Tetraodon nigroviridis"
            /db_xref="taxon:99883"
            /clone="015L14"
            /clone_lib="G"
            /note="Genoscope sequence ID : C0BG015DF07SP1-end :
            PUC-ori"

BASE COUNT  152 a      79 c      89 g      484 t      40 others
ORIGIN

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```
Query Match      13.3%; Score 55.2; DB 13; Length 844;
Best Local Similarity 46.4%; Pred. No. 0.26;
Matches 153; Conservative 7; Mismatches 170; Indels 0; Gaps 0;

QY 31 ttattgaaattttctgaatttaaaactgcatcaataaaawttatgttttctgctggacta 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158 TGAATTTAAATGTTATGATTTTCTTTAGAGTAAAGTTATATATTTTTCCTTTTAA 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 91 taaacactgactgttatttatcaataaataatttaaacatatattcttcaagatggga 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 TTTTAAATKGTATATATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 151 attaacatctacaaatgcctttcttcattgacacatgcacatccaccataataatt 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 GTTTTAAATTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 211 ataattataaactgaacacatgggccccctgctgttcacatgagatttcccgcta 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 338 TTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 271 ctattgtacgctgtatataccgataatgacatatatttatatgaacatgattaa 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 TAATATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 tgccttgagttgtctcaccgtaagagt 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 458 TTTTATTTACTTGTATTATGCGCAACACT 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
AQ745537/c
LOCUS
DEFINITION
  HS.2272.A2.B12.T7C CIT Approved Human Genomic Sperm Library D Homo
  sapiens genomic clone Plate-2272 Col-24 Row-C, DNA sequence.
ACCESSION
  AQ745537
VERSION
  AQ745537.1 GI:5523059
KEYWORDS
  GSS.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 845)
  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
  Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
  Hood,L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  99380589
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Clones may be purchased from Research Genetics (info@resgen.com).
  BAC end Web Server: http://www.htsc.washington.edu
  Plate: 2272 row: C column: 24
  Seq primer: T7
  Class: BAC ends
  High quality sequence stop: 845.
  Location/Qualifiers
    1..845
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="Plate-2272 Col-24 Row-C"
    /clone_lib="CIT Approved Human Genomic Sperm Library D"
    /sex="male"
    /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
    E-Coli DH10B"
BASE COUNT 360 a 114 c 93 g 278 t
```

ORIGIN

```
Query Match      13.3%; Score 55.2; DB 13; Length 845;
Best Local Similarity 47.9%; Pred. No. 0.26;
Matches 156; Conservative 1; Mismatches 169; Indels 0; Gaps 0;

QY 39 atattctgaaatttaaaactgcatcaataaaawttatgttttctgctggactaataact 98
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 99 gacttgatttttcaataaataatttaaacatatattcttcaagatgggaataaacat 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 ATATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 159 ctacaaattgcctttcttcattgacacatgcacatccaccataataataataattat 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 TTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 219 ataactgaaacatggtgccccctgctgttcacatgagatttctcgcgtactattgt 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 ATATATTTATATATATATATATATATATATATATATATATATATATATATATATAT 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 279 atacgtgtatatataccgataatgacatatatttatatgaacatgattgaatgcttg 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 TTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 339 agttgttctcaccgtaagagttica 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 ATACATGATAAAATGACAGACTTCCA 33

RESULT 9
CNS00K47
LOCUS
DEFINITION
  Drosophila melanogaster genome survey sequence TET3 end of BAC:
  BACR39E17 of RPCI-98 library from Drosophila melanogaster (fruit
  fly), genomic survey sequence.
ACCESSION
  AL077203
VERSION
  AL077203.1 GI:4956680
KEYWORDS
  GSS.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
  Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
  1 (bases 1 to 1101)
  Genoscope.
  Direct Submission
  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
  - Web : www.genoscope.cns.fr)
  Determination of this BAC-end sequence was carried out as part of a
  collaboration with the Berkeley Drosophila Genome Project (BDGP).
  The BDGP is constructing a physical map of the Drosophila
  melanogaster genome using these BACs. For further information
  please see http://www.fruitfly.org The BDGP Drosophila
  melanogaster BAC library was prepared by Kazutoyo Osoegawa and
  Aaron Mammoler in Pieter de Jong's laboratory in the Department of
  Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
  NY. The library is named RPCI-98 and was constructed by partial
  EcoRI digestion of Drosophila DNA provided by the BDGP from the
  isogenic strain y2; cn bw sp, the same strain used for the BDGP's
  pl and EST libraries. A more detailed description of the library
  and how to order individual BAC clones, the entire library, or
  filters for hybridization from the BACPAC Resource Center can be
  found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
  Location/Qualifiers
    1..1101
    /organism="Drosophila melanogaster"
    /db_xref="taxon:7227"
    /clone_lib="RPCI-98"
    /clone="BACR39E17"

FEATURES
  source
```


RESULT	14
CNS02A0C	
LOCUS	678 bp DNA GSS 12-MAY-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 249F10 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	ALU87941
VERSION	ALI87941.1 GI:7826045
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetraodon nigroviridis.
ORGANISM	Tetraodon nigroviridis. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodonta.
REFERENCE	1 (bases 1 to 678) Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
AUTHORS	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
TITLE	Unpublished
JOURNAL	2 (bases 1 to 678)
REFERENCE	Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
AUTHORS	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
TITLE	Unpublished
JOURNAL	3 (bases 1 to 678)
REFERENCE	Genoscope.
AUTHORS	

100 Jordan Hall, Clemson, SC 29634, USA


```
CC Tel: 864 656 7288
CC Fax: 864 656 4293
CC Email: rwing@clmson.edu
CC Seq primer: AATTAAACCTCACTAAAGGG
CC High quality sequence start: 38
CC High quality sequence stop: 1204.
XX
XX
FH Key Location/Qualifiers
FH
FT source 1..1337
FT /db_xref="taxon:4513"
FT /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"
FT /organism="Hordeum vulgare"
FT /cultivar="Morex"
FT /clone="HVSMEb0013H16f"
FT /clone_lib="Hordeum vulgare seedling shoot EST library
FT HVCdNA002 (Dehydration stress)"
FT /issue_type="Seedling shoot"
FT /lab_host="TJC121"
XX
SQ Sequence 1337 BP; 292 A; 22 C; 74 G; 941 T; 8 other;

Query Match 12.9%; Score 53.8; DB 5; Length 1337;
Best Local Similarity 51.2%; Pred. No. 0.44;
Matches 147; Conservative 1; Mismatches 135; Indels 4; Gaps 1;

QY 38 aatattctgaattaaacttgcataaataaattatgttttcttgctggactataacc 97
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 851 ATTATTTTATGATTAATAATCTTATCATCTGTTTTTGTGCTTTTTTATTTATT 910
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 98 tgacttgattttatcaataaataatttaaacatattcttccaagatgggaattaaca 157
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 911 TTAGTTATTTATTTATTTATGTTATTTATTTATTTATTTATTTATTTATTTAT 966
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 158 tctacaaattgcctttcttctatgcaccatgacatccctaccataaattataatta 217
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 967 TCATTATTTATTTTATTTTATTTTATTTTATTTATTTATTTATTTATTTATTTA 1026
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 218 tataactactgaaccatgggccctcgctgttacatgattctccgctactattg 277
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1027 TTATTTGTTTTTTTATTTTCATATTTTGATATTTATTTATTTATTTATTTAT 1086
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 278 tatacgtgtatatataccgtataatgacatatattttatgaacat 324
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1087 ATTTTATTTATTTATTTGTTATTTTANTATTTGTTATTTATTTATTTAT 1133
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: December 19, 2001, 17:00:33
Job time: 2275 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

QM nucleic - nucleic search, using sw model

Run on December 19, 2001, 17:31:51 ; Search time 230.16 Seconds
(without alignments)
1549.562 Million cell updates/sec

Title: US-09-698-903B-10
Perfect score: 416
Sequence: 1 ctgggcaatgtaccagctg.....catgaacaccccaactogat 416

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.*
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5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.*
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10: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.*
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12: /SID88/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT.*
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21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415.6	99.9	416	22	Left (3') border
2	380.8	91.5	415	22	Right (5') border
3	192.6	46.3	5864	17	Plasmid pCOLI13 T-
4	192.6	46.3	5865	22	Chimeric T-DNA of
5	192.6	46.3	7599	22	Nucleotide sequenc
6	190	45.7	5228	22	Plasmid pTsl72delt
7	190	45.7	6539	21	E. coli plasmid pT
8	190	45.7	6548	17	Plasmid pTsl74 use
9	190	45.7	6548	18	Plasmid pTsl72. C
10	190	45.7	6548	21	E. coli plasmid pT
11	190	45.7	7492	22	Plasmid pTsl346. U

12	189.6	45.6	1303	17	AAT39337	Plasmid pTsl88 (Eco
13	189.6	45.6	3201	12	AAH14529	pPS029 Bt ICP codi
14	189.6	45.6	4832	22	AAH25423	Nucleotide sequenc
15	189.6	45.6	4946	18	AAT59531	T-DNA of plasmid p
16	189.6	45.6	4946	22	AAH25422	Nucleotide sequenc
17	189.6	45.6	5349	19	AAV23339	T-DNA of pTTS24.
18	189.6	45.6	5864	17	AAT39339	Plasmid pCOLI13 T-
19	189.6	45.6	5865	22	AAH06990	Chimeric T-DNA of
20	189.6	45.6	7566	14	AAQ42160	Plasmid pPS0212 co
21	189.6	45.6	7639	14	AAQ42159	Plasmid pJD884 con
22	183.6	44.1	1037	11	AAQ04705	usp-promoter-casse
23	183.6	44.1	1085	11	AAQ04703	Legumin-signalpept
24	183.6	44.1	1160	11	AAQ04706	USP-signalpeptide
25	179	43.0	1077	22	AAH25439	Right flanking reg
26	176.6	42.5	3201	12	AAH15144	pVE36 Bt ICP codin
27	152.6	36.7	1186	13	AAQ25707	Chimeric neo gene
28	145.6	35.0	3153	21	AAZ29122	Plasmid pV131 comp
29	145.6	35.0	3336	21	AAZ29121	Plasmid pV130 comp
30	145.6	35.0	3694	21	AAZ29124	Plasmid pV133 used
31	145.6	35.0	3877	21	AAZ29123	Plasmid pV132 used
32	145.6	35.0	24593	6	AAH50226	Sequence of opine
33	145.6	35.0	24596	6	AAH50182	Complete nucleotid
34	104.6	25.1	936	22	AAF58252	Oligonucleotide D1
35	104.6	25.1	936	22	AAF58254	Oligonucleotide D1
36	104.6	25.1	936	22	AAF58257	Oligonucleotide D1
37	104.6	25.1	936	22	AAF58259	Oligonucleotide D2
38	104.6	25.1	936	22	AAF58262	Oligonucleotide D1
39	104.6	25.1	938	22	AAF58255	Oligonucleotide D1
40	104.2	25.0	936	22	AAF58252	Oligonucleotide D1
41	104.2	25.0	936	22	AAF58254	Oligonucleotide D1
42	104.2	25.0	936	22	AAF58257	Oligonucleotide D1
43	104.2	25.0	936	22	AAF58259	Oligonucleotide D2
44	104.2	25.0	936	22	AAF58262	Oligonucleotide D2
45	104.2	25.0	938	22	AAF58255	Oligonucleotide D1

ALIGNMENTS

RESULT	1
AAD06999	
ID	AAD06999 standard; DNA; 416 BP.
XX	
AC	AAD06999;
DT	
XX	06-AUG-2001 (first entry)
DE	Left (3') border flanking region of elite event MS-B2.
XX	MS-B2 elite event; transgenic Brassica plant; transformation event;
KW	male-sterility gene; ds.
KW	Chimeric - Agrobacterium sp.
XX	Chimeric - Brassica sp.
OS	
XX	
FH	Key Location/Qualifiers
FT	misc_feature 1..193
FT	/tag= a
FT	/note= "Corresponds to T-DNA"
FT	misc_feature 194..416
FT	/tag= b
FT	/note= "Corresponds to plant DNA"
XX	
XX	WO200131042-A2.
PN	
XX	03-MAY-2001.
PD	
XX	26-OCT-2000; 2000WO-EPI0680.
PF	
XX	29-OCT-1999; 99US-0430497.
PR	
XX	(AVET) AVENTIS CROPS SCIENCE NV.
PA	
XX	


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FT misc_feature 1...25
FT /tag= a
FT /note= "Right border repeat from the TL-DNA from
FT ptIB6S3"
FT 26...53
FT /tag= b
FT /note= "Synthetic polylinker derived sequence"
FT 54...90
FT /tag= c
FT /note= "Residual sequence from the TL-DNA at the
FT right border repeat"
FT 98...309
FT /tag= d
FT /note= "The 3' untranslated end from the TL-DNA
FT gene 7 (3'g7) of ptIB6S3"
FT 310...331
FT /tag= e
FT /note= "Synthetic polylinker derived sequence"
FT 332...883
FT /tag= f
FT /product= "Protein encoded by bialaphos resistance
FT gene (bar) of Streptomyces hygroscopicus"
FT 884...2609
FT /tag= g
FT /note= "Promoter from the atSIA ribulose-1,5-biphosphate
FT carboxylase small subunit gene from Arabidopsis thaliana"
FT 2610...2659
FT /tag= h
FT /note= "Synthetic polylinker derived sequence"
FT 2660...2920
FT /tag= i
FT /note= "TagI fragment from the 3' untranslated end of the
FT nopaline synthase gene (3'nos) from the T-DNA of pTi37
FT and containing plant polyadenylation signals"
FT 2921...2936
FT /tag= j
FT /note= "Synthetic polylinker derived sequence"
FT 2937...3032
FT /tag= k
FT /note= "The 3' untranslated region downstream from the
FT barnase coding sequence of Bacillus amyloliquefaciens"
FT 3033...3368
FT /tag= l
FT /product= "Protein encoded by barnase gene from
FT Bacillus amyloliquefaciens"
FT 3369...4878
FT /tag= m
FT /note= "Promoter region of the anther-specific gene
FT TA29 from Nicotiana tabacum"
FT 4879...4924
FT /tag= n
FT /note= "Synthetic polylinker derived sequence"
FT 4925...5215
FT /tag= o
FT /note= "Promoter of the nopaline synthase gene from the
FT T-DNA of pTi37 of Agrobacterium tumefaciens"
FT 5216...5217
FT /tag= p
FT /note= "Synthetic polylinker derived sequence"
FT 5218...5490
FT /tag= q
FT /product= "Protein encoded by barstar gene of
FT Bacillus amyloliquefaciens"
FT 5491...5530
FT /tag= r
FT /note= "Sequence from the 3' untranslated end of the
FT barstar gene from Bacillus amyloliquefaciens"
FT 5531...5554
FT /tag= s
FT /note= "Synthetic polylinker derived sequence"
FT 5555...5766
FT /tag= t
FT /note= "The 3' untranslated end from the TL-DNA
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FT misc_feature gene 7 (3'g7) of ptIB6S3"
FT /tag= u
FT /note= "Synthetic polylinker derived sequence"
FT 5774...5810
FT /tag= v
FT /note= "Residual sequence from the TL-DNA at the
FT right border repeat"
FT 5811...5840
FT /tag= w
FT /note= "Synthetic polylinker derived sequence"
FT 5841...5865
FT /tag= x
FT /note= "Left border repeat from the TL-DNA from
FT ptIB6S3"
FT
FT WO200131042-A2.
FT
FT 03-MAY-2001.
FT
FT 26-OCT-2000; 2000WO-EP10680.
FT
FT 29-OCT-1999; 99US-0430497.
FT (AVET ) AVENTIS CROPS SCIENCE NV.
FT
FT Weston B, De Beuckeleer M;
FT WPI; 2001-300517/31.
FT
FT Transgenic Brassica plants, seeds, cells or tissues, characterized by
FT harboring specific transformation events, particularly by presence of
FT male-sterility gene, at specific location in its genome -
FT
FT Claim 1; Page 47-49; 53pp; English.
FT
FT The present invention relates to a transgenic Brassica plant or its
FT seed, cells or tissues, characterised by harbouring a specific
FT transformation event, particularly by the presence of a male-sterility
FT gene, at a specific location in the Brassica genome. Transgenic
FT Brassica plant is useful for producing a hybrid seed by crossing the
FT transgenic plant with a male-fertile Brassica plant and harvesting the
FT hybrid seed from the transgenic Brassica plant.
FT The present sequence is chimeric T-DNA of plasmid pTCO113. This sequence
FT comprises right border repeat, left border repeat and 3' untranslated
FT region (UTR) from TL-DNA of ptIB6S3, synthetic polylinker sequences,
FT coding regions of bialaphos resistance gene (bar) from
FT streptomyces hygroscopicus, barnase gene from Bacillus amyloliquefaciens
FT and barstar gene from Bacillus amyloliquefaciens and promoters of atSIA
FT ribulose-1,5-biphosphate carboxylase small subunit gene from
FT Arabidopsis thaliana, the anther-specific gene TA29 from
FT Nicotiana tabacum and nopaline synthase gene from the T-DNA of pTi37
FT of Agrobacterium tumefaciens.
FT
FT Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
```

```
Query Match 46.3%; Score 192.6; DB 22; Length 5865;
Best Local Similarity 99.5%; Pred. No. 4.6e-30;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatatataatcagttattgaaatattctgaattaaacttgc 60
Db 5621 ctacggcaatgtaccagctgatatataatcagttattgaaatattctgaattaaacttgc 5680
QY 61 atcaataaaawttatgttttctgttgactataataacacctgacttattttatcaataaa 120
Db 5681 atcaataaaawttatgttttctgttgactataataacacctgacttattttatcaataaa 5740
QY 121 tatttaaaactatattcttctcaagatgggaattacaactacaatctcatttcatttc 180
Db 5741 tatttaaaactatattcttctcaagatgggaattacaactacaatctcatttcatttc 5800
```

QY 181 gaccatgtacatc 193
 Db 5801 gaccatgtacatc 5813

RESULT 5
 AAF25320
 ID AAF25320 standard; DNA; 7599 BP.
 XX
 AC AAF25320;
 DT 30-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of a plasmid PGKBS.

XX Plant promoter; root cell; root-specific expression; parasite resistance;
 KW nematode resistance; fungal resistance; water stress; salt stress;
 KW sugar content; nitrogen transport; ss.
 XX Synthetic.

XX WO200100833-A1.
 PN 04-JAN-2001.
 PD 23-JUN-2000; 2000WO-FR01768.
 XX 25-JUN-1999; 99FR-0008185.
 PR (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA Hoffmann B, Mollier P, Pelletier G;
 PI WPI; 2001-102893/11.
 DR
 XX
 XX New constitutive plant promoter active specifically in roots, useful
 PT for controlling expression of pest or drought resistance genes, and
 PT related transgenic plants -
 XX
 PS Disclosure; Fig 9; 92pp; French.

XX The present sequence represents a plasmid PGKBS. The plasmid contains
 CC a plant promoter that directs expression of a selected sequence in
 CC root cells at all stages of development of a plant. The plant promoter
 CC is used to control expression of genes in a root-specific manner,
 CC especially genes that provide resistance to parasites, pests (nematodes
 CC or fungi), water and salt stress, or alter sugar content or nitrogen
 CC transport. Fragments of the promoter are useful as probes or primers
 CC to detect or amplify at least part of the promoter.

XX Sequence 7599 BP; 1972 A; 1938 C; 1937 G; 1752 T; 0 other;

Query Match 46.3%; Score 192.6; DB 22; Length 7599;
 Best Local Similarity 99.5%; Pred. No. 4.6e-40;
 Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataacagttattgaaatttctgaatttaaaactgc 60
 Db 6579 ctacggcaatgtaccagctgataataacagttattgaaatttctgaatttaaaactgc 6638
 QY 61 atcaataaaawttatgttttctgttgactataaacctgactgtgtattttatcaataaa 120
 Db 6639 atcaataaaawttatgttttctgttgactataaacctgactgtgtattttatcaataaa 6698
 QY 121 tatttaaacatattttcttcaagatgggaattaaacatctacaattgcctttcttcatc 180
 Db 6699 tatttaaacatattttcttcaagatgggaattaaacatctacaattgcctttcttcatc 6758

QY 181 gaccatgtacatc 193
 Db 6759 gaccatgtacatc 6771

RESULT 6
 AAF86439
 ID AAF86439 standard; DNA; 5228 BP.
 XX
 AC AAF86439;
 XX
 DT 25-JUN-2001 (first entry)
 XX
 DE Plasmid pTSl72delta.
 XX
 KW Male sterile plant; RNAase inhibitor; plasmid pTSl72delta; ds.

XX Unidentified.
 OS
 XX WO200124616-A1.
 PN 12-APR-2001.
 PD 12-SEP-2000; 2000WO-JP06222.
 XX 30-SEP-1999; 99JP-0279307.
 PR (NISB) JAPAN TOBACCO INC.
 PA Hamada K, Nakakido F;
 XX WPI; 2001-266212/27.

XX Method for producing male sterile rice and maize by inserting RNAase
 PT gene and RNAase inhibitor genes with promoters into the plant genome -
 PT Disclosure; Page 14-17; 29pp; Japanese.
 XX The present invention relates to a method for producing male sterile
 CC plants. The method comprises inserting a promoter fragment upstream of an
 CC RNAase gene and a second promoter, upstream of an RNAase inhibitor protein
 CC gene and inserting it into the plant genome. The method is useful for
 CC producing male sterile tobacco, lettuce and rapeseed plants, but
 CC preferably rice and maize. The present sequence is a vector used in
 CC the method of the present invention.

XX Sequence 5228 BP; 1384 A; 1307 C; 1263 G; 1274 T; 0 other;
 Query Match 45.7%; Score 190; DB 22; Length 5228;
 Best Local Similarity 99.0%; Pred. No. 1.5e-29;
 Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataacagttattgaaatttctgaatttaaaactgc 60
 Db 5031 ctacggcaatgtaccagctgataataacagttattgaaatttctgaatttaaaactgc 5090
 QY 61 atcaataaaawttatgttttctgttgactataaacctgactgtgtattttatcaataaa 120
 Db 5091 atcaataaaawttatgttttctgttgactataaacctgactgtgtattttatcaataaa 5150
 QY 121 tatttaaacatattttcttcaagatgggaattaaacatctacaattgcctttcttcatc 180
 Db 5151 tatttaaacatattttcttcaagatgggaattaaacatctacaattgcctttcttcatc 5210
 QY 181 gaccatgtacat 192
 Db 5211 gaccatgtacat 5222

RESULT 7
 AAZ91097
 ID AAZ91097 standard; DNA; 6539 BP.
 XX
 AC AAZ91097;
 XX
 DT 06-JUN-2000 (first entry)

XX DE E. coli plasmid pTS431 containing mutant barnase gene.
 XX KW Male sterile plant; mutant barnase gene; anther-specific expression;
 KW low fidelity PCR; primer; plant breeding; ss.
 XX OS Synthetic.
 XX PN WO200008176-A1.
 XX PD 17-FEB-2000.
 XX PF 03-AUG-1999; 99WO-JP04167.
 XX PR 04-AUG-1998; 98JP-0220060.
 XX PA (NISR) JAPAN TOBACCO INC.
 XX PI Hamada K, Nakakido F;
 XX DR WPI; 2000-195581/17.
 XX PD
 XX PF Mutate barnase gene for efficient construction of plant transformants,
 PF particularly male sterile plants free from any undesirable characters
 PF by specifically expressing the gene alone in anther.
 XX PS Example 3; Page 23-27; 30pp; Japanese.
 XX QC The invention relates to the generation of male sterile plants by
 QC the introduction of a mutant barnase gene (AAZ91095) for expression
 QC specifically in the anther of a plant. This sequence represents the
 QC E. coli/Agrobacterium shuttle vector plasmid pTS172 which contains
 QC the mutated barnase gene (AAZ91095) under control of the cauliflower
 QC mosaic virus 35S promoter. The vector also contains a region of the
 CC Agrobacterium T-DNA gene 7. The vector is used for transmitting the
 CC barnase gene to plants via an Agrobacterium tumefaciens host cell.
 CC The transformed plant is used in plant breeding.
 XX SQ Sequence 6539 BP; 1755 A; 1578 C; 1519 G; 1687 T; 0 other;

Query Match 45.7%; Score 190; DB 21; Length 6539;
 Best Local Similarity 99.0%; Pred. No. 1.5e-29;
 Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataatcagttattgaaatattctgaatttaaaacttgc 60
 Db |||||||
 6342 ctacggcaatgtaccagctgataatcagttattgaaatattctgaatttaaaacttgc 6401
 QY 61 atcaataaaattatgtttttgttgactataatcactgactgttattttatcaataaa 120
 Db |||||||
 6402 atcaataaaattatgtttttgttgactataatcactgactgttattttatcaataaa 6461
 QY 121 tatttaaaactatattcttccaagatgggaattaaacatacacaattgcctttttatc 180
 Db |||||||
 6462 tatttaaaactatattcttccaagatgggaattaaacatacacaattgcctttttatc 6521
 QY 181 gaccatgtacat 192
 Db |||||||
 6522 gaccatgtacgt 6533

RESULT 8
 ID AAT39336
 XX AAT39336 standard; DNA; 6548 BP.
 AC AAT39336;
 XX
 XX 22-JAN-1997 (first entry)
 DE Plasmid pTS174 used to obtain male sterile rice.
 XX Plasmid pTS174; male sterile; barnase; ribonuclease; transgenic plant;

KW rice; Oryza sativa; ds; cyclic.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH misc_feature 1..2003
 FT /tag= a
 FT /label= Vector
 FT /note= "pUC19 derived vector sequences"
 FT complement (2019..2283)
 FT /tag= b
 FT /label= 3'nos
 FT /note= "region containing polyadenylation signal
 FT nopaline synthase gene of Agrobacterium
 FT T-DNA"
 FT complement (2284..2624)
 FT /tag= c
 FT /label= Barnase
 FT /product= Bacillus amyloliquefaciens barnase
 FT complement (2625..4313)
 FT /tag= d
 FT /label= PEI
 FT /function= promoter of the stamen-specific E1 gene
 FT Of rice
 FT 4336..5710
 FT /tag= e
 FT /label= P35S
 FT /function= 35S promoter of cauliflower mosaic virus
 FT 5711..6262
 FT /tag= f
 FT /label= bar
 FT /product= phosphinothricin acetyltransferase
 FT 6263..6496
 FT /tag= g
 FT /label= 3'g7
 FT /function= region containing polyadenylation signal
 XX
 PN WO9626283-A1.
 XX 29-AUG-1996.
 XX 21-FEB-1996; 96WO-EP00722.
 XX 21-FEB-1995; 95EP-0400364.
 XX (PLBZ) PLANT GENETIC SYSTEMS NV.
 PI Botterman J, Cornelissen M, Michiels F;
 DR WPI; 1996-402373/40.
 XX Prodn. of male sterile plants by transforming with a chimaeric
 construct comprising a male sterility DNA e.g. barnase and a
 co-regulating gene, e.g. barstar, into the nuclear genome, useful
 for generating hybrid cultivars
 XX Example 1; Page 33-37; 56pp; English.
 PS Plasmid pTS174 (AAT39336) contains Bacillus barnase DNA under control
 CC of the stamen-specific PEI promoter. Embryogenic callus from rice
 CC cv. Kochinbiki was transformed with pTS174 alone or with pTS88
 CC (see also AAT39337), a plasmid contg. barstar DNA under control of a
 CC 35S promoter. With pTS174 alone, 1 male sterile line was recovered
 CC from 48 electroporation cuvettes. With both plasmids, 7 normal
 CC male sterile lines were recovered from 40 cuvettes. Barnase
 CC expression disturbed the function of stamen cells leading to male
 CC sterility. Constitutive expression of barstar counteracted any low
 CC level expression of barnase in non-stamen tissue.
 XX Sequence 6548 BP; 1757 A; 1578 C; 1523 G; 1690 T; 0 other;

Query Match 45.7%; Score 190; DB 17; Length 6548;

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Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacgcaatgtaccagctataataacagctattgaaatatttctgaatttaaaacttgc 60
Db 6351 ctacgcaatgtaccagctataataacagctattgaaatatttctgaatttaaaacttgc 6410

QY 61 atcaataaaawttatgttttctggtgactataataacacgtgacttgttatttatacaataaa 120
Db 6411 atcaataaaawttatgttttctggtgactataataacacgtgacttgttatttatacaataaa 6470

QY 121 tatttaaacataattttctcaagatgggaataaacaataacataacaaatgacctttcttcttc 180
Db 6471 tatttaaacataattttctcaagatgggaataaacaataacataacaaatgacctttcttcttc 6530

QY 181 gaccatgtacat 192
Db 6531 gaccatgtacgt 6542

RESULT 9
AAAT61394
ID AAAT61394 standard; DNA; 6548 BP.
XX AC AAAT61394;
XX DT 07-MAY-1997 (first entry)
XX DE Plasmid pTS172.
XX KW Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP;
KW niacinamide; Agrobacterium; T-DNA; male sterile; barnase;
KW ribonuclease; RNase; cereal; wheat; Triticum aestivum;
XX plasmid pTS172; ds.
XX OS Chimeric Agrobacterium sp.;
OS Chimeric Oryza sativa;
OS Chimeric cauliflower mosaic virus.
XX FH Location/Qualifiers
FT 3'UTR complement (2019..2288)
FT /*tag= a
FT /label= 3'nos
FT /note= "3' untranslated region contg. the poly-A
FT signal of Agrobacterium T-DNA nopaline
FT CDS complement (2289..2624)
FT /*tag= b
FT /product= barnase
FT complement (2625..4313)
FT /*tag= c
FT /label= pE1
FT /note= "promoter region of rice El gene"
FT promoter complement (4336..5710)
FT /*tag= d
FT /label= p35S
FT /note= "35S promoter region of cauliflower mosaic
FT virus"
FT CDS 5711..6262
FT /*tag= e
FT /label= Bar
FT /note= "phosphinothricin acetyltransferase"
FT 3'UTR 6243..6496
FT /*tag= f
FT /label= 3'g7
FT /note= "3' untranslated region contg. the poly-A
FT signal of gene 7 of Agrobacterium T-DNA"
XX PN EP757102-A1.
XX PD 05-FEB-1997.
XX PP 04-AUG-1995; 95EP-0401844.

XX 04-AUG-1995; 95EP-0401844.
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX De Block M;
XX WPI; 1997-111050/11.
XX Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase
XX inhibitor - reduces the cultured cells response to stress and
XX reduces metabolism
XX Example 2; Page 17-20; 25pp; English.
XX Plasmid pTS172 (AAAT61394) contains the barnase coding sequence under
XX control of the rice El gene stamen-specific promoter and a
XX phosphinothricin acetyltransferase coding sequence under control of
XX the CaMV 35S promoter. Plasmid pTS172 and plasmid pTS772 (see also
XX AAAT61395) were used to transform wheat Spring variety Pavon calli via
XX particle bombardment. Some calli were treated with the poly-(ADP-
XX ribose) polymerase inhibitor niacinamide before, or before and
XX after, bombardment. Healthy, male sterile plants were regenerated
XX only from bombarded calli that were treated with niacinamide. This
XX was believed to be due to more faithful expression characteristics
XX of the integrated stamen-selective barnase gene in these calli
XX and regenerated shoots. For plants transformed with pTS172,
XX foreign DNA was stably incorporated in the wheat genome in 2-3
XX copies.
XX SQ Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;

Query Match 45.7%; Score 190; DB 18; Length 6548;
Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacgcaatgtaccagctataataacagctattgaaatatttctgaatttaaaacttgc 60
Db 6351 ctacgcaatgtaccagctataataacagctattgaaatatttctgaatttaaaacttgc 6410

QY 61 atcaataaaawttatgttttctggtgactataataacacgtgacttgttatttatacaataaa 120
Db 6411 atcaataaaawttatgttttctggtgactataataacacgtgacttgttatttatacaataaa 6470

QY 121 tatttaaacataattttctcaagatgggaataaacaataacataacaaatgacctttcttcttc 180
Db 6471 tatttaaacataattttctcaagatgggaataaacaataacataacaaatgacctttcttcttc 6530

QY 181 gaccatgtacat 192
Db 6531 gaccatgtacgt 6542

RESULT 10
AAZ91096
ID AAZ91096 standard; DNA; 6548 BP.
XX AC AAZ91096;
XX DT 06-JUN-2000 (first entry)
XX DE E. coli plasmid pTS172 containing synthetic barnase gene.
XX KW Male sterile plant; mutant barnase gene; anther-specific expression;
XX low fidelity PCR; primer; plant breeding; ss.
XX OS Synthetic.
XX PN WO200008176-A1.
XX PD 17-FEB-2000.
XX PP 04-AUG-1995; 95EP-0401844.
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PF 03-AUG-1999; 99WO-JP04167.
XX
PR 04-AUG-1998; 99JP-0220060.
XX
PA (NISR ) JAPAN TOBACCO INC.
XX
PI Hamada K, Nakakido F;
XX WPI; 2000-195581/17.
XX
PT Mutate barnase gene for efficient construction of plant transformants,
PT particularly male sterile plants free from any undesirable characters
PT by specifically expressing the gene alone in anther.
XX
PS Example 3; Page 19-23; 30pp; Japanese.
XX
CC The invention relates to the generation of male sterile plants by
CC the introduction of a mutant barnase gene (AAZ91095) for expression
CC specifically in the anther of a plant. This sequence represents the
CC E. coli/Agrobacterium shuttle vector plasmid pRS172 which contains
CC the synthetic barnase gene (AAZ91094) under control of the cauliflower
CC mosaic virus 35S promoter. The vector also contains a region of the
CC Agrobacterium T-DNA gene 7. The vector is used for transmitting the
CC barnase gene to plants via an Agrobacterium tumefaciens host cell.
CC The transformed plant is used in plant breeding.
XX
SQ Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;

Query Match 45.7%; Score 190; DB 21; Length 6548;
Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaacttgc 60
DB 6351 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaacttgc 60
QY 61 atcaataaaattatgttttcttgctgactataataactgactgttatttatcaataaa 120
DB 6411 atcaataaaattatgttttcttgctgactataataactgactgttatttatcaataaa 120
QY 121 tatttaaacatatttttttccaagatgggaattacaatctacaaattgccttttttattc 180
DB 6471 tatttaaacatatttttttccaagatgggaattacaatctacaaattgccttttttattc 180
QY 181 gaccatgtacat 192
DB 6531 gaccatgtacgt 6542

RESULT 11
AAF86441
ID AAF86441 standard; DNA; 7492 BP.
XX
AC AAF86441;
XX
DT 25-JUN-2001 (first entry)
XX
DE Plasmid pTS346.
XX
KW Male sterile plant; RNAase inhibitor; plasmid pTS346; ds.
XX
OS Unidentified.
XX
PN WO200124616-A1.
XX
PD 12-APR-2001.
XX
PF 12-SEP-2000; 2000WO-JP06222.
XX
PR 30-SEP-1999; 99JP-0279307.
XX
PA (NISR ) JAPAN TOBACCO INC.

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XX Hamada K, Nakakido F;
XX WPI; 2001-266212/27.
XX
PT Method for producing male sterile rice and maize by inserting RNase
PT gene and RNase inhibitor genes with promoters into the plant genome -
XX
PS Disclosure; Page 19-23; 29pp; Japanese.
XX
CC The present invention relates to a method for producing male sterile
CC plants. The method comprises inserting a promoter fragment upstream of an
CC RNase gene and a second promoter, upstream of an RNase inhibitor protein
CC gene and inserting it into the plant genome. The method is useful for
CC producing male sterile tobacco, lettuce and rapeseed plants, but
CC preferably rice and maize. The present sequence is a vector used in
CC the method of the present invention.
XX
SQ Sequence 7492 BP; 1987 A; 1801 C; 1752 G; 1952 T; 0 other;

Query Match 45.7%; Score 190; DB 22; Length 7492;
Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaacttgc 60
DB 7295 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaacttgc 60
QY 61 atcaataaaattatgttttcttgctgactataataactgactgttatttatcaataaa 120
DB 7355 atcaataaaattatgttttcttgctgactataataactgactgttatttatcaataaa 120
QY 121 tatttaaacatatttttttccaagatgggaattacaatctacaaattgccttttttattc 180
DB 7415 tatttaaacatatttttttccaagatgggaattacaatctacaaattgccttttttattc 180
QY 181 gaccatgtacat 192
DB 7475 gaccatgtacgt 7486

RESULT 12
AAT39337
ID AAT39337 standard; DNA; 1303 BP.
XX
AC AAT39337;
XX
DT 22-JAN-1997 (first entry)
XX
DE Plasmid pTS88 (EcoRI-HindIII fragment).
XX
KW Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
KW transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..35
FT /tag= a
FT /label= pGEM2
FT /note= "polylinker of pGEM2"
FT promoter 36..694
FT /tag= b
FT /label= p35S
FT /function= 35S promoter of cauliflower mosaic virus
FT CDS 695..967
FT /tag= c
FT /label= barstar
FT /product= Bacillus amyloliquefaciens barstar
FT polyA_signal 968..1287
FT /tag= d

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RESULT	13
AAQ14529	
ID	AAQ14529 standard; DNA; 3201 BP.
XX	
AC	AAQ14529;
XX	
DT	27-JAN-1992 (first entry)
XX	
DE	pfs029 Bt ICF coding sequence.

DE Nucleotide sequence of plasmid pTHW118.

Db	183	ATCAATAAAATTATGTTTTTTCGTTGGACTATAATACCTGACTTGTATTATTTTATCAATAAAA	124
Qy	121	tatttaaacatattctttccaagatgggaatcaacatctacaaaattgccttttcttcttc	180
Db	123	TATTTAAACTATATTCTTTCAAGATGGGAATTAAACATCTACAAATGGCCTTTTCTTATC	64
Qy	181	gaccatgtac	190
Db	63	GACCATGTAC	54

Search completed: December 19, 2001, 17:32:10
Job time: 4167 sec

PN	EPF57102-A1.	
PP		
PD	05-FEB-1997.	
PE		
PF	04-AUG-1995; 95EP-0401844.	
PG		
PH	04-AUG-1995; 95EP-0401844.	
PI		
PJ	(PLBZ) PLANT GENETIC SYSTEMS NV.	
PK		
PL	De Block M;	
PM		
PN	WPI; 1997-111050/11.	
PO		
PP	Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase	
PQ	inhibitor - reduces the cultured cells response to stress and	
PR	reduces metabolism	
PS	Example 3; Page 13-16; 25pp; English.	
PT		
PV		
PW		
PX		
PY		
PZ		
QA	Plasmid pTHW107 is a vector carrying T-DNA (AAT59531) comprising a	
QB	barase coding sequence under control of the tobacco TA29 gene	
QC	stamen-specific promoter and a phosphinothricin acetyltransferase	
QD	coding sequence under control of an Arabidopsis Rubisco small	
QE	subunit gene promoter. Oilseed rape hypocotyl explants were	
QF	infected with Agrobacterium tumefaciens C58C1Rif carrying vector	
QG	pTHW107 and helper Ti plasmid pMP60. In some treatments, the	
QH	hypocotyls were treated with the poly-(ADP-ribose) polymerase	
QI	inhibitor niacinamide (250 mg/l) 4 days prior to infection.	
QJ	Plants regenerated from niacinamide-treated transformed calli	
QK	had a low copy number and displayed less variation in the	
QL	expression profile of the transgenes.	
QM		
QN	Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;	
QO		

Query Match	45.6%	Score 189.6;	DB 18;	Length 4946;
Best Local Similarity	99.5%;	Pred. No. 1.18e-29;		
Matches 189;	Conservative	1;	Mismatches 0;	Indels 0;
			Gaps	0;

1 ctacggcaatgtaccagctgataataatcagttattgaatatattctgaatttaaacctgc 60
|||||
243 CTACGGCAATGTACCAGCTGATAATATCAGTTATTGAAATATTCTGAATTTAAACTGC 184
|||
61 atcaataaawttatgtttttctgttggaactataatacactgactgtgttattttatcaataa 120

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 17:27:49 ; Search time 1631.12 Seconds
(without alignments)
4207.432 Million cell updates/sec

Title: US-09-698-903B-10

Perfect score: 416

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248599755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba:*

2: gb_hgt:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pi:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vi:*

30: em_htgo_hum:*

31: em_htgo_inv:*

32: em_htgo_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB	ID	Description
1	415.6	99.9	416	6	AX127757	AX127757 Sequence
2	380.8	91.5	415	6	AX127755	AX127755 Sequence
3	192.6	46.3	585	6	AX127748	AX127748 Sequence
4	192.6	46.3	7599	6	AX063413	AX063413 Sequence
5	190.45	45.7	6539	6	E31991	E31991 Mutated bar
6	190.45	45.7	6548	6	A60109	A60109 Sequence 2
7	190.45	45.7	6548	6	A76916	A76916 Sequence 2
8	190.45	45.7	6548	6	AR098308	AR098308 Sequence
9	190.45	45.7	6548	6	E31990	E31990 Mutated bar
10	190.45	45.7	7811	6	AR078675	AR078675 Sequence
11	189.6	45.6	3200	6	I44104	I44104 Sequence 23
12	189.6	45.6	4832	6	AX172441	AX172441 Sequence
13	189.6	45.6	4946	6	A60108	A60108 Sequence 1
14	189.6	45.6	4946	6	A76915	A76915 Sequence 1
15	189.6	45.6	4946	6	AR098307	AR098307 Sequence
16	189.6	45.6	4946	6	AX172440	AX172440 Sequence 7
17	189.6	45.6	5349	6	A71437	A71437 Sequence 7
18	189.6	45.6	5560	6	A60112	A60112 Sequence 5
19	189.6	45.6	5560	6	AR098311	AR098311 Sequence
20	189.6	45.6	5855	6	AX127748	AX127748 Sequence
21	189.6	45.6	7566	6	A24783	A24783 plasmid pPS
22	189.6	45.6	7566	6	AR074388	AR074388 Sequence
23	189.6	45.6	7639	6	A24782	A24782 plasmid pJD
24	189.6	45.6	7639	6	AR074387	AR074387 Sequence
25	183.6	44.1	1037	6	A10942	A10942 Nucleotide
26	183.6	44.1	1085	6	A10939	A10939 Nucleotide
27	183.6	44.1	1160	6	A10943	A10943 Nucleotide
28	179.43	43.0	1077	6	AX172463	AX172463 Sequence
29	176.6	42.5	3201	6	I44103	I44103 Sequence 22
30	154.6	37.2	2476	12	TBI251013	AJ251013 Transform
31	154.6	37.2	3236	12	TBI251014	AJ251014 Transform
32	152.6	36.7	1186	6	A18051	A18051 DNA used as
33	152.6	36.7	1186	6	AR095107	AR095107 Sequence
34	152.6	36.7	1186	6	AR098313	AR098313 Sequence
35	152.6	36.7	1186	6	AX012338	AX012338 Sequence
36	152.6	36.7	1186	6	I49886	I49886 Sequence 2
37	152.6	36.7	1186	6	I82374	I82374 Sequence 2
38	152.6	36.7	12095	12	BINHYGDA	Z37515 Binary vect
39	146.2	35.1	878	1	ATTDNA	X00431 Agrobacteri
40	145.6	35.0	831	1	ATTNR7	V00090 Agrobacteri
41	145.6	35.0	24595	1	ATACH5	X00493 Agrobacteri
42	145.6	35.0	24595	6	E00404	E00404 Ti plasmid
43	145.6	35.0	24595	6	E00546	E00546 DNA fragmen
44	145.6	35.0	194140	1	AF242881	AF242881 Agrobacte
45	116	27.9	249	12	ARGMTUB	X05579 Soybean bet

ALIGNMENTS

RESULT 1
AX127757
LOCUS AX127757 416 bp DNA
DEFINITION Sequence 10 from Patent WO0131042.
ACCESSION AX127757 PAT 15-MAY-2001
VERSION AX127757.1 GI:14134404
KEYWORDS
SOURCE .
ORGANISM
synthetic construct.
synthetic construct.
artificial sequence.
1 (bases 1 to 416)
REFERENCE
AUTHORS Weston,B. and de Beuckeleer,M.
TITLE Male-sterile brassica plants and methods for producing same
JOURNAL Patent: WO 0131042-A 10 03-MAY-2001;
Aventis CropScience N.V. (BE)
FEATURES
source Location/Qualifiers
1. .416
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="3' border flanking region of elite event MS-B2"

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misc_feature 1..193
/note="r-DNA"
misc_feature 194..416
/note="plant DNA"
BASE COUNT 137 a 72 c 152 t 1 others
ORIGIN
1 ctacggcaatgtaccagctgatatataatcagttattgaaatatttctgaatttaaaacttgc 60
|||||
415 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTCAATTTAAACTTGC 356
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61 atcaataaawttatgttttcttgctggactataataacacctgacttgctttatttatacaataa 120
|||||
355 ATCAATAAATTTAGTTTTCTTGGACTATAATACCTGACTTGTGTTATTTTATCAATAAAA 296
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121 tatttaaacatattttcttcaagatgggaattaaacatctacaaattgcctttcttctatc 180
|||||
295 TATTAAACATATATTCTTCAAGATGGGAATTAACATCTACAAATTCCTTTCTTATC 236
|||||
181 gaccatgtacatcctacacataaattataaattataataataacacacacacacacacacac 239
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235 GGCCATGTACATCCTACCAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 176
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240 cccctgctgtttacatggatttctcgcgtactatttctgatacgtgtatataacacacacac 299
|||||
175 CCCTGCTGCTTTACATGGATTTCTTCGGCTACATTTTGTATACGTGTATATA-TA-CGTAT 117
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300 atgtacatatatttatgaacatgatttaattgctgtgagttgcttctcaccgttaagag 359
|||||
116 AATGTACATATATTATATGAACATGATTAAATGCTGTGAGTTGTTCTCATCGTAAAGAG 57
|||||
360 ttccaatatgaatgctgaagctcaaaacacacacacacacacacacacacacacacacacac 409
|||||
56 TTCAATATGTAATGTTGAAGAGTCAAAACCCAAATCATGAACACCCAAA 7

RESULT 3
AX127748
LOCUS AX127748 5865 bp DNA PAT 15-MAY-2001
DEFINITION Sequence 1 from Patent WO0131042.
ACCESSION AX127748
VERSION AX127748.1 GI:14134395
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
ARTIFICIAL SEQUENCE.
REFERENCE 1 (bases 1 to 5865)
AUTHORS Weston,B. and de Beuckeleer,M.
TITLE Male-sterile brassica plants and methods for producing same
JOURNAL Patent: WO 0131042-A 1 03-MAY-2001;
Aventis CropScience N.V. (BE)
FEATURES
source 1..5865
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="r-DNA of plasmid pCOL13"
BASE COUNT 1849 a 1095 c 1149 g 1772 t
ORIGIN
Query Match 46.3%; Score 192.6; DB 6; Length 5865;
Best Local Similarity 99.5%; Pred. No. 1.3e-24;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 ctacggcaatgtaccagctgatatataatcagttattgaaatatttctgaatttaaaacttgc 60
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5621 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTCAATTTAAACTTGC 5680
|||||
61 atcaataaawttatgttttcttgctggactataataacacctgacttgctttatttatacaataa 120
|||||
5681 ATCAATAAATTTAGTTTTCTTGGACTATAATACCTGACTTGTGTTATTTTATCAATAAAA 5740
|||||
121 tatttaaacatattttcttcaagatgggaattaaacatctacaaattgcctttcttctatc 180
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5741 TATTAAACATATATTCTTCAAGATGGGAATTAACATCTACAAATTCCTTTCTTATC 5800
|||||
181 gaccatgtacatc 193
|||||
5801 GACCATGTACATC 5813
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RESULT 4
AX063413
LOCUS AX063413 7599 bp DNA PAT 24-JAN-2001
DEFINITION Sequence 5 from Patent WO0100833.
ACCESSION AX063413
VERSION AX063413.1 GI:12541201
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 7599)
AUTHORS Hoffmann,B., Mollner,P. and Pelletier,G.
TITLE Promoter expressed specifically in the cells of plant roots,
recombinant vectors and host cells comprising same and transgenic
plants obtained
JOURNAL Patent: WO 0100833-A 5 04-JAN-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR)
FEATURES
source Location/Qualifiers
BASE COUNT 1972 a 1938 c 1937 g 1752 t
ORIGIN
Query Match 46.3%; Score 192.6; DB 6; Length 7599;
Best Local Similarity 99.5%; Pred. No. 1.3e-24;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaaacttgc 60
DB 6579 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6638
QY 61 atcaataaaawttatgttttctgctggactataataacctgactgttattttatcaataaaa 120
DB 6639 ATCAATAAAATTTATGTTTTGCTTGGACTATAATACCTGACTTGTATTATCAATAAAA 6698
QY 121 tatttaaacatattttcttcaagatgggaattaaacatctacaaatgcctttcttctatc 180
DB 6699 TATTAAACTATATTCTTTTCAAGATGGGAATTAACATCTACAAATTTGCCCTTTCTTATC 6758
QY 181 gaccatgtacatc 193
DB 6759 GACCATGTACATC 6771
RESULT 5
LOCUS E31991 6539 bp DNA PAT 07-FEB-2001
DEFINITION Mutated barnase gene and transgenic plant thereof.
ACCESSION E31991
VERSION E31991.1 GI:13021588
KEYWORDS JP 2000041682-A/4.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 6539)
AUTHORS Kazuyuki,H.F.N.N.
TITLE Mutated barnase gene and transgenic plant thereof
JOURNAL Patent: JP 2000041682-A 4 15-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Escherichia coli LE392
PN JP 2000041682-A/4
PD 15-FEB-2000
PF 04-AUG-1998 JP 1998220060
PR
PI KAZUYUKI HAMADA,FUMIO NAKAKIDO
PC C12N15/09,A01H5/00,C12N5/10,C12N9/22/(C12N5/10,C12R1:91), PC
C12N15/00,
PC C12N5/00,(C12N5/00,C12R1:91)
CC

FH Key Location/Qualifiers
FT source 1..6539 /organism="Escherichia coli LE392".
FEATURES
source Location/Qualifiers
BASE COUNT 1755 a 1578 c 1519 g 1687 t
ORIGIN
Query Match 45.7%; Score 190; DB 6; Length 6539;
Best Local Similarity 99.0%; Pred. No. 3.6e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaaacttgc 60
DB 6342 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6401
QY 61 atcaataaaawttatgttttctgctggactataataacctgactgttattttatcaataaaa 120
DB 6402 ATCAATAAAATTTATGTTTTGCTTGGACTATAATACCTGACTTGTATTATCAATAAAA 6461
QY 121 tatttaaacatattttcttcaagatgggaattaaacatctacaaatgcctttcttctatc 180
DB 6462 TATTAAACTATATTCTTTTCAAGATGGGAATTAACATCTACAAATTTGCCCTTTCTTATC 6521
QY 181 gaccatgtacat 192
DB 6522 GACCATGTACGT 6533
RESULT 6
LOCUS A60109 6548 bp DNA circular PAT 22-OCT-1999
DEFINITION Sequence 2 from Patent WO9706267.
ACCESSION A60109
VERSION A60109.1 GI:3715125
KEYWORDS
SOURCE Plasmid PTS172.
ORGANISM Plasmid PTS172.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De,B.M.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: WO 9706267-A 2 20-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
FEATURES
source Location/Qualifiers
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN
Query Match 45.7%; Score 190; DB 6; Length 6548;
Best Local Similarity 99.0%; Pred. No. 3.6e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaaacttgc 60
DB 6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6410
QY 61 atcaataaaawttatgttttctgctggactataataacctgactgttattttatcaataaaa 120
DB 6411 ATCAATAAAATTTATGTTTTGCTTGGACTATAATACCTGACTTGTATTATCAATAAAA 6470
QY 121 tatttaaacatattttcttcaagatgggaattaaacatctacaaatgcctttcttctatc 180
DB 6471 TATTAAACTATATTCTTTTCAAGATGGGAATTAACATCTACAAATTTGCCCTTTCTTATC 6530
QY 181 gaccatgtacat 192
DB 6533 GACCATGTACGT 6548

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Db 6531 GACCATGTACGT 6542

RESULT 7
A76916 6548 bp DNA circular PAT 22-OCT-1999
DEFINITION Sequence 2 from Patent EP0757102.
ACCESSION A76916
VERSION A76916.1 GI:6088713
KEYWORDS Plasmid pTS172.
SOURCE Plasmid pTS172.
ORGANISM Plasmids.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De,B.M.
TITLE GENETIC TRANSFORMATION USING A PARP INHIBITOR
JOURNAL Patent: EP 0757102-A 2 05-FEB-1997;
PLANT GENETIC SYSTEMS NW (BE)
FEATURES
    source      Location/Qualifiers
    source      1. .6548
                /organism="Plasmid pTS172"
                /db_xref="taxon:106340"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN
Query Match 45.7%; Score 190; DB 6; Length 6548;
Best Local Similarity 99.0%; Pred. No. 3.6e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatatttctgaattttaaacttgc 60
Db 6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6410
QY 61 atcaataaaawttatgttttcttgagactataataactgactgttatttattcaataaa 120
Db 6411 ATCAATAAAATTTATGTTTGGCTTGGACTATAATACTGACTTGTATTATTAATAATAA 6470
QY 121 tattaaactatatttcttcaagatgggaattacaatctacaaattgcctttcttacc 180
Db 6471 TATTTAACTATATTCTTCAAGATGGGAATTAACATCTACAAATTCCTTTCTTATC 6530
QY 181 gaccatgtacat 192
Db 6531 GACCATGTACGT 6542

RESULT 9
E31990 6548 bp DNA PAT 07-FEB-2001
DEFINITION Mutated barnase gene and transgenic plant thereof.
ACCESSION E31990
VERSION E31990.1 GI:13021587
KEYWORDS JP 2000041682-A/3.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 6548)
AUTHORS Kazuyuki, H.F.N.N.
TITLE Mutated barnase gene and transgenic plant thereof
JOURNAL Patent: JP 2000041682-A 3 15-FEB-2000;
COMMENT JAPAN TOBACCO INC
        OS Escherichia coli LE392
        PN JP 2000041682-A/3
        PD 15-FEB-2000
        PF 04-AUG-1998 JP 19982220060
        PR
        PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
        PC C12N15/09, A01H5/00, C12N5/10, C12N9/22, (C12N5/10, C12N1:91), PC
        C12N15/00,
        PC C12N5/00, (C12N5/00, C12N1:91)
        CC
        FH Key Location/Qualifiers
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FEATURES
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    source      1. .6548
                /organism="unidentified"
                /db_xref="taxon:32644"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN
Query Match 45.7%; Score 190; DB 6; Length 6548;
Best Local Similarity 99.0%; Pred. No. 3.6e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatatttctgaattttaaacttgc 60
Db 6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6410
QY 61 atcaataaaawttatgttttcttgagactataataactgactgttatttattcaataaa 120
Db 6411 ATCAATAAAATTTATGTTTGGCTTGGACTATAATACTGACTTGTATTATTAATAATAA 6470
QY 121 tattaaactatatttcttcaagatgggaattacaatctacaaattgcctttcttacc 180
Db 6471 TATTTAACTATATTCTTCAAGATGGGAATTAACATCTACAAATTCCTTTCTTATC 6530
QY 181 gaccatgtacat 192
Db 6531 GACCATGTACGT 6542

RESULT 8
AR098308 6548 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6074876.
ACCESSION AR098308
VERSION AR098308.1 GI:12807565
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De Block,M.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: US 6074876-A 2 13-JUN-2000;
FEATURES
    source      Location/Qualifiers
    source      1. .6548
                /organism="unknown"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN
Query Match 45.7%; Score 190; DB 6; Length 6548;
Best Local Similarity 99.0%; Pred. No. 3.6e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatatttctgaattttaaacttgc 60
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RESULT 10
AR078675/c
LOCUS AR078675 7811 bp DNA PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5962768.
ACCESSION AR078675
VERSION AR078675.1 GI:10005421
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7811)
AUTHORS Cornelissen,M., Reynaerts,A., Gossele,V. and Van Aarssen,R.
TITLE Marker gene
JOURNAL Patent: US 5962768-A 5 05-OCT-1999;
FEATURES
    source
        1..7811
            /organism="unknown"
BASE COUNT 1950 a 1906 c 1873 g 2082 t
ORIGIN

Query Match 45.7%; Score 190; DB 6; Length 7811;
Best Local Similarity 99.0%; Pred. No. 3.5e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgatataatcagttattgaaattttctgaatttaaaacttgc 60
    |||||||
Db 629 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTCGAATTTAAACTTGC 570
    |||||||

Qy 61 atcaataaawttatgttttctgctggactataataacacgtactgtttatttatcaataaa 120
    |||||||
Db 569 ATCAATAAATTTATGTTTCTGCTGGACTATAATACCTGACTCTGTTTATTATCAATAAAA 510
    |||||||

Qy 121 tatttaaacatattttctcaagatgggaattaaacatctacaaattgcctttcttctatc 180
    |||||||
Db 509 TATTTAACTATATTCTTTCAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 450
    |||||||

Qy 181 gaccatgtacat 192
    |||||||
Db 449 GACCATGTACGT 438
    |||||||

RESULT 11
I44104
LOCUS I44104 3200 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 23 from patent US 5633446.
ACCESSION I44104
VERSION I44104.1 GI:2469202
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3200)
AUTHORS Cornelissen,M., Soetaert,P., Stam,M. and Dockx,J.
TITLE Modified Bacillus thuringiensis insecticidal-crystal protein genes and their expression in plant cells
JOURNAL Patent: US 5633446-A 23 27-MAY-1997;
FEATURES
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        1..3200
            /organism="unknown"
BASE COUNT 880 a 710 c 720 g 885 t
ORIGIN

Query Match 45.6%; Score 189.6; DB 6; Length 3200;
Best Local Similarity 99.5%; Pred. No. 4.5e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgatataatcagttattgaaattttctgaatttaaaacttgc 60
    |||||||
Db 2952 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTCGAATTTAAACTTGC 3011
    |||||||

Qy 61 atcaataaawttatgttttctgctggactataataacacgtactgtttatttatcaataaa 120

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Db 3012 ATCAATAAATTTATGTTTTCCTTGGACTATAATACCTGACTTGTATTATTTATCAATAAA 3071
    |||||||
Qy 121 tatttaaacatattttctcaagatgggaattaaacatctacaaattgcctttcttctatc 180
    |||||||
Db 3072 TATTTAAACTATATTCTTTCACAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 3131
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Qy 181 gaccatgtac 190
    |||||||
Db 3132 GACCATGTAC 3141
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RESULT 12
AX172441/c
LOCUS AX172441 4832 bp DNA PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0141558.
ACCESSION AX172441
VERSION AX172441.1 GI:14597553
KEYWORDS
    synthetic construct.
    ORGANISM synthetic construct
    REFERENCE 1 (bases 1 to 4832)
    AUTHORS de Both,G. and de Beuckeleer,M.
    TITLE Hybrid winter oilseed rape and methods for producing same
    JOURNAL Patent: WO 0141558-A 2 14-JUN-2001;
    FEATURES
        Location/Qualifiers
            source
                1..4832
                    /organism="synthetic construct"
                    /db_xref="taxon:32630"
                    /note="T-DNA of plasmid pTHW118"
            misc_feature
                1883..4065
                    /note="HpaI restriction fragment"
BASE COUNT 1528 a 883 c 932 g 1488 t
ORIGIN

Query Match 45.6%; Score 189.6; DB 6; Length 4832;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgatataatcagttattgaaattttctgaatttaaaacttgc 60
    |||||||
Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTCGAATTTAAACTTGC 184
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Qy 61 atcaataaawttatgttttctgctggactataataacacgtactgtttatttatcaataaa 120
    |||||||
Db 183 ATCAATAAATTTATGTTTTCCTTGGACTATAATACCTGACTTGTATTATTTATCAATAAA 124
    |||||||

Qy 121 tatttaaacatattttctcaagatgggaattaaacatctacaaattgcctttcttctatc 180
    |||||||
Db 123 TATTTAACTATATTCTTTCACAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 64
    |||||||

Qy 181 gaccatgtac 190
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Db 63 GACCATGTAC 54
    |||||||

RESULT 13
A60108/c
LOCUS A60108 4946 bp DNA PAT 06-MAR-1998
DEFINITION Sequence 1 from Patent WO9706267.
ACCESSION A60108
VERSION A60108.1 GI:3715124
KEYWORDS
    Transformation vector pTHW107.
    ORGANISM Transformation vector pTHW107
    REFERENCE 1 (bases 1 to 4946)
    AUTHORS De,B.N.
    TITLE Genetic transformation using a PARP inhibitor
    JOURNAL Patent: WO 9706267-A 1 20-FEB-1997;

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PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
1. .4946
/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
BASE COUNT 1569 a 891 c 963 g 1523 t
ORIGIN

Query Match 45.6%; Score 189.6; DB 6; Length 4946;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaaacttgc 60
Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 184
QY 61 atcaataaawttatgttttgcctggactataataacctgactgttattttatcaataaa 120
Db 183 ATCAATAAATTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATCAATAAA 124
QY 121 tatttaaacatattctttcgaagtgggaattaaacatctacaaattgcctttcttattc 180
Db 123 TATTTAAACTATATTTCTTCAAGATGGGAATTAACATCTACAAATTCGCTTTCTTATC 64
QY 181 gaccatgtac 190
Db 63 GACCATGTAC 54

RESULT 14
A76915/c
LOCUS 4946 bp DNA PAT 19-OCT-1999
DEFINITION Sequence 1 from Patent EP0757102.
ACCESSION A76915
VERSION A76915.1 GI:6088712
KEYWORDS Transformation vector pTHW107.
SOURCE Transformation vector pTHW107.
ORGANISM Transformation vector pTHW107.
REFERENCE 1 (bases 1 to 4946)
AUTHORS De B.M.
TITLE Genetic transformation using a PARP INHIBITOR
JOURNAL Patent: EP 0757102-A 1 05-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
1. .4946
/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
BASE COUNT 1569 a 891 c 963 g 1523 t
ORIGIN

Query Match 45.6%; Score 189.6; DB 6; Length 4946;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaaacttgc 60
Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 184
QY 61 atcaataaawttatgttttgcctggactataataacctgactgttattttatcaataaa 120
Db 183 ATCAATAAATTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATCAATAAA 124
QY 121 tatttaaacatattctttcgaagtgggaattaaacatctacaaattgcctttcttattc 180
Db 123 TATTTAAACTATATTTCTTCAAGATGGGAATTAACATCTACAAATTCGCTTTCTTATC 64
QY 181 gaccatgtac 190
Db 63 GACCATGTAC 54

PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
1. .4946
/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
BASE COUNT 1569 a 891 c 963 g 1523 t
ORIGIN

Query Match 45.6%; Score 189.6; DB 6; Length 4946;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaaacttgc 60
Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 184
QY 61 atcaataaawttatgttttgcctggactataataacctgactgttattttatcaataaa 120
Db 183 ATCAATAAATTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATCAATAAA 124
QY 121 tatttaaacatattctttcgaagtgggaattaaacatctacaaattgcctttcttattc 180
Db 123 TATTTAAACTATATTTCTTCAAGATGGGAATTAACATCTACAAATTCGCTTTCTTATC 64
QY 181 gaccatgtac 190
Db 63 GACCATGTAC 54
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RESULT 15
AR098307/c
LOCUS 4946 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6074876.
ACCESSION AR098307
VERSION AR098307.1 GI:12807564
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4946)
AUTHORS De Block, M.
TITLE Genetic transformation using a PARP Inhibitor
JOURNAL Patent: US 6074876-A 1 13-JUN-2000;
FEATURES
source
1. .4946
/organism="unknown"
BASE COUNT 1569 a 891 c 963 g 1523 t
ORIGIN
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Query Match 45.6%; Score 189.6; DB 6; Length 4946;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaaacttgc 60
Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 184
QY 61 atcaataaawttatgttttgcctggactataataacctgactgttattttatcaataaa 120
Db 183 ATCAATAAATTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATCAATAAA 124
QY 121 tatttaaacatattctttcgaagtgggaattaaacatctacaaattgcctttcttattc 180
Db 123 TATTTAAACTATATTTCTTCAAGATGGGAATTAACATCTACAAATTCGCTTTCTTATC 64
QY 181 gaccatgtac 190
Db 63 GACCATGTAC 54
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Search completed: December 19, 2001, 17:28:06
Job time: 3928 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 17:33:57 ; Search time 110.23 Seconds
(without alignments)
854.711 Million cell updates/sec

Title: US-09-698-903b-10
Perfect score: 416
Sequence: 1 ctacggcaatgtaccagctg.....catgaacaccccaactcgat 416

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 11328999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192.6	46.3	5864	3	US-08-894-440-4
2	190	45.7	6548	3	US-08-894-440-1
3	190	45.7	6548	3	US-08-817-188-2
4	189.6	45.6	7811	2	US-08-549-680A-5
5	189.6	45.6	1303	3	US-08-894-440-2
6	189.6	45.6	3200	1	US-08-453-104-23
7	189.6	45.6	3200	2	US-08-694-824-23
8	189.6	45.6	4946	3	US-08-817-188-1
9	189.6	45.6	5560	3	US-08-817-188-5
10	189.6	45.6	7566	2	US-08-232-016-23
11	189.6	45.6	7639	2	US-08-232-016-22
12	188	45.2	5834	3	US-08-894-440-4
13	176.6	42.5	3201	2	US-08-453-104-22
14	176.6	42.5	3201	2	US-08-694-824-22
15	152.6	36.7	1186	1	US-08-064-121-2
16	152.6	36.7	1186	1	US-08-478-015-2
17	152.6	36.7	1186	3	US-08-475-975-2
18	152.6	36.7	1186	3	US-09-084-889-2
19	145.6	35.0	3153	4	US-09-080-625-3
20	145.6	35.0	3336	4	US-09-080-625-2
21	145.6	35.0	3694	4	US-09-080-625-5
22	145.6	35.0	3877	4	US-09-080-625-4
23	142.6	34.3	24595	6	5428147-1
24	51.2	12.3	80246	4	US-09-078-294-4
25	50.4	12.1	80595	4	US-09-078-294-3
26	41.8	10.0	19124	2	US-08-487-826B-13
27	41.4	10.0	15397	2	US-08-673-768-1

c	28	41.4	10.0	15397	2	US-08-673-768-1	Sequence 1, Appli
c	29	41.4	10.0	24595	6	5428147-1	Patent No. 5428147
c	30	40.4	9.7	80246	4	US-09-078-294-4	Sequence 4, Appli
c	31	40.2	9.7	289	4	US-09-007-005-17	Sequence 17, Appl
c	32	40.2	9.7	289	4	US-09-244-796-17	Sequence 17, Appl
c	33	40	9.6	1588	3	US-09-058-489-45	Sequence 45, Appl
c	34	39.8	9.6	665	2	US-08-883-795A-36	Sequence 36, Appl
c	35	39	9.4	9048	3	US-08-973-273-4	Sequence 4, Appli
c	36	38.8	9.3	1800	3	US-08-617-860B-23	Sequence 23, Appl
c	37	38.6	9.3	3947	4	US-08-975-762-47	Sequence 47, Appl
c	38	38.6	9.3	3947	4	US-09-295-028-47	Sequence 47, Appl
c	39	38.6	9.3	3947	4	US-09-106-582-47	Sequence 47, Appl
c	40	37.6	9.0	1056	1	US-08-402-217A-1	Sequence 1, Appli
c	41	37.6	9.0	1056	1	US-08-700-178-1	Sequence 1, Appli
c	42	37.6	9.0	1056	3	US-08-995-654-1	Sequence 1, Appli
c	43	37.4	9.0	8654	1	US-08-920-812-6	Sequence 6, Appli
c	44	37.4	9.0	8654	1	US-08-920-812-6	Sequence 6, Appli
c	45	37.4	9.0	8654	1	US-08-921-177-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-894-440-4
; Sequence 4, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5864
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pTColl3
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((98)..(330))
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((331)..(882))
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((883)..(2608))
; OTHER INFORMATION: promoter of small subunit gene of Rubisco of
; OTHER INFORMATION: Arabidopsis (Pssu)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2659)..(3031))
; OTHER INFORMATION: region containing polyadenylation signal of
; OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
; OTHER INFORMATION: (3'nos)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((3032)..(3367))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: Complement((3368)..(4877))
; OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4924)..(5216)
; OTHER INFORMATION: promoter of nopaline synthase gene of
; OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5217)..(5489)
; OTHER INFORMATION: region coding for barstar of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5490)..(5765)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA
; US-08-894-440-4

Query Match      46.3%; Score 192.6; DB 3; Length 5864;
Best Local Similarity 99.5%; Pred. No. 1.4e-35;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  '1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaattttaaacttgc 60
Db  5620 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaattttaaacttgc 5679
QY  61 atcaataaaatttattgttttctgttgactataataactgactgttattttatcaataaa 120
Db  5680 atcaataaaatttattgttttctgttgactataataactgactgttattttatcaataaa 5739
QY  121 tatttaaacataattttcttccaagatgggaattacaatctacaaattgcctttcttattc 180
Db  5740 tatttaaacataattttcttccaagatgggaattacaatctacaaattgcctttcttattc 5799
QY  181 gaccatgtacatc 193
Db  5800 gaccatgtacatc 5812

RESULT 2
US-08-894-440-1
; Sequence 1, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
; NAME/KEY: misc_feature
; LOCATION: (1)..(2003)
; OTHER INFORMATION: pUC19 derived vector sequences (vector)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2283)..(2289))
; OTHER INFORMATION: 3' nos: region containing polyadenylation signal
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; OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2284)..(2624))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: promoter of the stamen-specific EI gene of rice
; OTHER INFORMATION: (PEI)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4336)..(5710)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5711)..(6262)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: region containing polyadenylation signal to gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; US-08-894-440-1
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Query Match      45.7%; Score 190; DB 3; Length 6548;
Best Local Similarity 99.0%; Pred. No. 5.7e-35;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaattttaaacttgc 60
Db  6351 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaattttaaacttgc 6410
QY  61 atcaataaaatttattgttttctgttgactataataactgactgttattttatcaataaa 120
Db  6411 atcaataaaatttattgttttctgttgactataataactgactgttattttatcaataaa 6470
QY  121 tatttaaacataattttcttccaagatgggaattacaatctacaaattgcctttcttattc 180
Db  6471 tatttaaacataattttcttccaagatgggaattacaatctacaaattgcctttcttattc 6530
QY  181 gaccatgtacat 192
Db  6531 gaccatgtacgt 6542
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```
RESULT 3
US-08-817-188-2
; Sequence 2, Application US/08817188
; Patent No. 6074876
; GENERAL INFORMATION:
; APPLICANT: DE BLOCK, MARC
; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
; FILE REFERENCE: 2121-0127P
; CURRENT APPLICATION NUMBER: US/08/817,188
; CURRENT FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: PCT/EP96/03366
; EARLIER FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: EP 95401844.6
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS172
; NAME/KEY: misc_feature
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US-08-894-440-2

; Sequence 2, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1303
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HindIII-EcORI
; OTHER INFORMATION: fragment of pRS8
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(35)
; OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36)..(694)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
; OTHER INFORMATION: CM1841 (P35S)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (695)..(967)
; OTHER INFORMATION: region coding for barstar of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (968)..(1287)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1288)..(1303)
; OTHER INFORMATION: polylinker of pGEM2

US-08-894-440-2

Query Match 45.6%; Score 189.6; DB 3; Length 1303;
Best Local Similarity 99.5%; Pred. No. 6e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttatgaaataattctgaatttaaaacttgc 60
|||||
Db 1098 ctacggcaatgtaccagctgataataatcagttatgaaataattctgaatttaaaacttgc 1157
QY 61 atcaataaaawttatgtttttgttggtgactataataacctgactgtttattttatcaataaa 120
|||||
Db 1158 atcaataaaawttatgtttttgttggtgactataataacctgactgtttattttatcaataaa 1217
QY 121 tatttaaacctattcttctcaagatgggaataataacatctacaaattgcctttttatc 180
|||||
Db 1218 tatttaaacctattcttctcaagatgggaataataacatctacaaattgcctttttatc 180
QY 181 gaccatgtac 190
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Db 1278 gaccatgtac 1287

RESULT 6

US-08-453-104-23
; Sequence 23, Application US/08453104
; Patent No. 5633446
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke

; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,104
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."

US-08-453-104-23

Query Match 45.6%; Score 189.6; DB 1; Length 3200;
Best Local Similarity 99.5%; Pred. No. 6.5e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttatgaaataattctgaatttaaaacttgc 60
|||||
Db 2952 ctacggcaatgtaccagctgataataatcagttatgaaataattctgaatttaaaacttgc 3011
QY 61 atcaataaaawttatgtttttgttggtgactataataacctgactgtttattttatcaataaa 120
|||||
Db 3012 atcaataaaawttatgtttttgttggtgactataataacctgactgtttattttatcaataaa 3071
QY 121 tatttaaacctattcttctcaagatgggaataataacatctacaaattgcctttttatc 180
|||||
Db 3072 tatttaaacctattcttctcaagatgggaataataacatctacaaattgcctttttatc 3131
QY 181 gaccatgtac 190
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Db 3132 gaccatgtac 3141

RESULT 7

US-08-694-824-23
; Sequence 23, Application US/08694824
; Patent No. 5877306

GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETART, Piet
APPLICANT: STAM, Maïke
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Burns, Doane, Swecker & Mathis
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22131-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2078..2082
OTHER INFORMATION: /note= "Nucleotides 2078-2082
OTHER INFORMATION: wherein N is not known."
US-08-694-824-23

Query Match 45.6%; Score 189.6; DB 2; Length 3200;
Best Local Similarity 99.5%; Pred. No. 6.5e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaatttaaaactgc 60
Db 2952 CTACGGCAATGTACCAGCTGATATATCAGTATTGAATATTCTGAAATTTAAACTGC 3011
QY 61 atcaataaaatgtatgttttgcctggactataataactgactgttattttatcaataaa 120
Db 3012 ATCAATAAATTTATGTTTGTCTGGACTATATACCTGACTTGTATTATTTATCAATAA 3071
QY 121 tatttaaacatattcttccaagatgggaattacaatctacaaatgcctttcttatc 180
Db 3072 TATTAAACATATATTCTTTCAAGATGGGAATTAACATCTACAAATGCGCTTTCTTATC 3131
QY 181 gaccatgtac 190
Db 3132 GACCATGTAC 3141

RESULT 8
US-08-817-188-1/c
Sequence 1, Application US/08817188
Patent No. 6074876
GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4946
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
OTHER INFORMATION: plasmid pTHW107
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((97)..(330))
OTHER INFORMATION: 3' g7: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: bar: region coding for phosphinotricin acetyl
OTHER INFORMATION: transferase
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter region of Rubisco small subunit gene of
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2658)..(3031))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4876))
OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((4922)..(4946))
OTHER INFORMATION: LB: T-DNA left border
US-08-817-188-1

Query Match 45.6%; Score 189.6; DB 3; Length 4946;
Best Local Similarity 99.5%; Pred. No. 6.8e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaatttaaaactgc 60
Db 243 CTACGGCAATGTACCAGCTGATATATCAGTATTGAATATTCTGAAATTTAAACTGC 184

QY 61 atcaataaawttatgtttttgttgactataataacctgactgttattttatcaataaa 120
 Db 183 ATCAATAAATTTATGTTTGTGCTGACTATAATACCTGACTGTATTTATCAATAA 124
 QY 121 tattaaactatttcttcaagatgggaattacacatctacaaattgcctttcttacc 180
 Db 123 TATTAACTATATCTCTTCAAGATGGGAATTAACTACTACAAATGCCCTTTCTTATC 64
 QY 181 gaccatgtac 190
 Db 63 GACCATGTAC 54

RESULT 9

US-08-817-188-5/c
 ; Sequence 5, Application US/08817188
 ; Patent No. 6074876
 ; GENERAL INFORMATION:
 ; APPLICANT: DE BLOCK, MARC
 ; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
 ; FILE REFERENCE: 2121-0127P
 ; CURRENT APPLICATION NUMBER: US/08/817,188
 ; CURRENT FILING DATE: 1997-05-15
 ; EARLIER APPLICATION NUMBER: PCT/EP96/03366
 ; EARLIER FILING DATE: 1996-07-31
 ; EARLIER APPLICATION NUMBER: EP 95401844.6
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 5560
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
 ; OTHER INFORMATION: plasmid pTHW142
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(25)
 ; OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from
 ; OTHER INFORMATION: pT186S3
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (84)..(296)
 ; OTHER INFORMATION: 3' q7: 3' untranslated region containing the
 ; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
 ; OTHER INFORMATION: T-DNA
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (318)..(869)
 ; OTHER INFORMATION: bar: region coding for phosphinotricin
 ; OTHER INFORMATION: acetyltransferase
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (830)..(2760)
 ; OTHER INFORMATION: PSSU: promoter region of Rubisco small subunit
 ; OTHER INFORMATION: gene of Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (2765)..(3058)
 ; OTHER INFORMATION: 3' untranslated region of the CamV 35S transcript
 ; OTHER INFORMATION: containing polyadenylation signals
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (3059)..(5056)
 ; OTHER INFORMATION: uidA: region coding for beta-glucuronidase
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (4483)..(4671)
 ; OTHER INFORMATION: IV2: region corresponding to the second intron of
 ; OTHER INFORMATION: the ST-LS1 gene
 ; FEATURE:
 ; NAME/KEY: misc_feature

; LOCATION: (5067)..(5502)
 ; OTHER INFORMATION: P35S: 35S promoter region of CamV
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5533)..(5560)
 ; OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
 ; OTHER INFORMATION: pT186S3
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5058)..(5059)
 ; OTHER INFORMATION: region with unknown sequence (may contain up to 20
 ; OTHER INFORMATION: nucleotides)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5077)..(5078)
 ; OTHER INFORMATION: region with unknown sequence (may contain up to 20
 ; OTHER INFORMATION: nucleotides)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5476)..(5479)
 ; OTHER INFORMATION: region with unknown sequence (may contain up to 20
 ; OTHER INFORMATION: nucleotides)
 ; US-08-817-188-5

Query Match 45.6%; Score 189.6; DB 3; Length 5560;
 Best Local Similarity 99.5%; Pred. No. 6.9e-35;
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatatataatcaagttattgaaatattctgaatttaaaacttgc 60
 Db 230 CTACGGCAATGTACCAGCTGATATATCAGTTATTGGAATATTTCTGAATTTAAACTTGC 171
 QY 61 atcaataaawttatgtttttgttgactataataacctgactgttattttatcaataaa 120
 Db 170 ATCAATAAATTTATGTTTGTGCTGACTATAATAACCTGACTGTGTTATTTATCAATAA 111
 QY 121 tattaaactatttcttcaagatgggaattacacatctacaaattgcctttcttacc 180
 Db 110 TATTAACTATATTTCTTCAAGATGGGAATTAACTACTACAAATGCCCTTTCTTATC 51
 QY 181 gaccatgtac 190
 Db 50 GACCATGTAC 41

RESULT 10

US-08-232-016-23
 ; Sequence 23, Application US/08232016
 ; Patent No. 5952547
 ; GENERAL INFORMATION:
 ; APPLICANT: CORNELISSEN, Marc
 ; APPLICANT: SOETAERT, Piet
 ; APPLICANT: STAM, Maïke
 ; APPLICANT: DOCKX, Jan
 ; APPLICANT: VAN AARSEN, Roel
 ; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,016

FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: plasmid DNA designated as pPS0212
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1785
OTHER INFORMATION: /note= "Coding region of a truncated modified bt2 (cryIAB) gene, also designated as the cryIAB6 gene."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA gene 7."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2396..2921
OTHER INFORMATION: /note= "35S promoter sequence derived from Cauliflower mosaic virus."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of chloramphenicol acetyl transferase gene."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3582..4407
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA octopine synthase gene."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5600..5657
OTHER INFORMATION: /note= "Sequence complementary to the coding sequence of the beta-lactamase gene."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7071..7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter derived from Agrobacterium T-DNA (with modified leader with respect to sequence of pJD884 of SEQ ID NO. 22)."
US-08-232-016-23
Query Match 45.6%; Score 189.6; DB 2; Length 7566;
Best Local Similarity 99.5%; Pred. No. 7.1e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgataataatcagttatttgaataattcttgaatttaacttgc 60
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Db 1881 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAATATTCTGAATTTAAACTTGC 1940
QY 61 atcaataaawttatgttttctgctggactataatcacctgactgtgttttttatacaataaa 120
|||||
Db 1941 ATCAATAAATTTATGTATTTTCTGGACTATAATACCTGACTTCTTATTTTATCAATAAA 2000
QY 121 tatttaaacatatttcttcaagatgggaattacacatctacaataatgcctttcttctatc 180
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Db 2001 TATTAAACATATATTCTTCAAGATGGGAATTAACATCTACAATAATGCCCTTTCTTATC 2060
QY 181 gaccatgtac 190
|||||
Db 2061 GACCATGTAC 2070
RESULT 11
US-08-232-016-22
Sequence 22, Application US/08232016
Patent No. 5952547
GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maïke
APPLICANT: DOCKX, Jan
APPLICANT: VAN AARSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 7639 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: plasmid DNA designated as pJD884
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1869
OTHER INFORMATION: /note= "Coding region of a truncated bt2 (cryIAB) gene, also designated as the bt884
FEATURE:
NAME/KEY: misc_feature

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; LOCATION: 1877..2110
; OTHER INFORMATION: /note= "3' regulatory sequence
; OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA gene 7."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2480..3005
; OTHER INFORMATION: /note= "35S promoter sequence
; OTHER INFORMATION: derived from Cauliflower mosaic virus."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3006..3665
; OTHER INFORMATION: /note= "Coding sequence of
; OTHER INFORMATION: chloramphenicol acetyl transferase gene."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3666..4491
; OTHER INFORMATION: /note= "3' regulatory sequence
; OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA octopine synthase gene."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5684..6541
; OTHER INFORMATION: /note= "Sequence complementary to
; Patent No. 5952547
; OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7155..7639
; OTHER INFORMATION: /note= "TR1' and TR2' promoter
; OTHER INFORMATION: derived from Agrobacterium T-DNA."
; US-08-232-016-22

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Query Match 45.6%; Score 189.6; DB 2; Length 7639;
Best Local Similarity 99.5%; Pred. No. 7.1e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaatttaaacctgc 60
Db 1965 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 2024

QY 61 atcaataaawttatgttttctgctggactataatacctgactgtattttatcaataaa 120
Db 2025 ATCAATAAATTTATGTTTCTGCTGGACATAATACCTGACTGTATTTTATCAATAAA 2084

QY 121 tatttaaacctattcttctcaagatgggaataacatctacaaatgcctttcttcttc 180
Db 2085 TATTTAACTATATTCTTTCAAGATGGGAATTAACATCTACAAATTGCTTTTCTTATC 2144

QY 181 gaccatgtac 190
Db 2145 GACCATGTAC 2154

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RESULT 12
US-08-894-440-4/c
; Sequence 4, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5864
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of

```

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; OTHER INFORMATION: plasmid pTCO113
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((98)..(330))
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((331)..(882))
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((883)..(2608))
; OTHER INFORMATION: promoter of small subunit gene of Rubisco of
; OTHER INFORMATION: Arabidopsis (pssu)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2659)..(3031))
; OTHER INFORMATION: region containing polyadenylation signal of
; OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
; OTHER INFORMATION: (3'nos)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((3032)..(3367))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((3368)..(4877))
; OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
; OTHER INFORMATION: tabacum (PTA29)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4924)..(5216)
; OTHER INFORMATION: promoter of nopaline synthase gene of
; OTHER INFORMATION: Agrobacterium T-DNA (Phos)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5217)..(5489)
; OTHER INFORMATION: region coding for barstar of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5490)..(5765)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA
; US-08-894-440-4

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Query Match 45.2%; Score 188; DB 3; Length 5864;
Best Local Similarity 98.9%; Pred. No. 1.6e-34;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaatttaaacctgc 60
Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 184

QY 61 atcaataaawttatgttttctgctggactataatacctgactgtattttatcaataaa 120
Db 183 ATCAATAAATTTATGTTTCTGCTGGACTATAATACCTGACTTGTATTATCAATAAA 124

QY 121 tatttaaacctattcttctcaagatgggaataacatctacaaatgcctttcttcttc 180
Db 123 TATTTAACTATATTCTTTCAAGATGGGAATTAACATCTACAAATTGCTTTTCTTATC 64

```

Qy 181 gaccatgtac 190
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Db 63 GACCATGTAC 54

RESULT 13

US-08-453-104-22

; Sequence 22, Application US/08453104

; Patent No. 5633446

; GENERAL INFORMATION:

; APPLICANT: CORNELISSEN, Marc

; APPLICANT: SOETAERT, Piet

; APPLICANT: STAM, Maïke

; APPLICANT: DOCKX, Jan

; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS

; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

; TITLE OF INVENTION: IN PLANT CELLS

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: George Mason Bldg., Washington & Prince Sts.

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/453,104

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,869

; FILING DATE: 16-DEC-1992

; APPLICATION NUMBER: GB 90401055.0

; FILING DATE: 18-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa S

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 010830-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3201 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 2151..2155

; OTHER INFORMATION: /note= "Nucleotides 2151-2155

; OTHER INFORMATION: wherein N is not known."

US-08-453-104-22

Query Match 42.5%; Score 176.6; DB 1; Length 3201;
Best Local Similarity 99.4%; Pred. No. 5.7e-32;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgataataacagttattgaaatatttctgaatttaaacctgc 60
|||||
Db 3025 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAAATTTAAACTTGC 3084

Qy 61 atcaataaaawttatgcttctggactataataacacgtactgttattttatcaataaa 120
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Db 3085 ATCAATAAAWTTATGCTTCTGGACTATAATAACCTGACTTGTATTATTTATCAATAAA 3144

Qy 121 tatttaaacatatatttcttcaagatgggaattacaatctctacaatgcctttctt 177
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Db 3145 TATTTAAACTATATTCTTCAAGATGGGAATTAAACATCTACAAATTCGCTTTTCTT 3201

RESULT 14

US-08-694-824-22

; Sequence 22, Application US/08694824

; Patent No. 5877306

; GENERAL INFORMATION:

; APPLICANT: CORNELISSEN, Marc

; APPLICANT: SOETAERT, Piet

; APPLICANT: STAM, Maïke

; APPLICANT: DOCKX, Jan

; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS

; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

; TITLE OF INVENTION: IN PLANT CELLS

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: George Mason Bldg., Washington & Prince Sts.

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/694,824

; FILING DATE: 09-AUG-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,869

; FILING DATE: 16-DEC-1992

; APPLICATION NUMBER: GB 90401055.0

; FILING DATE: 18-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa S

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 010830-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3201 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 2151..2155

; OTHER INFORMATION: /note= "Nucleotides 2151-2155

; OTHER INFORMATION: wherein N is not known."

US-08-694-824-22

Query Match 42.5%; Score 176.6; DB 2; Length 3201;
Best Local Similarity 99.4%; Pred. No. 5.7e-32;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgataataacagttattgaaatatttctgaatttaaacctgc 60
|||||
Db 3025 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAAATTTAAACTTGC 3084

Qy 61 atcaataaaawttatgcttctggactataataacacgtactgttattttatcaataaa 120
|||||
Db 3085 ATCAATAAAWTTATGCTTCTGGACTATAATAACCTGACTTGTATTATTTATCAATAAA 3144

Qy 121 tatttaaacatatttttcaagatggggaattaaacatctacaaattgccttttctt 177
|||||
Db 3145 TATTAAACTATATTCTTCAAGATGGGAATTAAACATCTACAAATGGCTTTCTT 3201
|||||

RESULT 15
US-08-064-121-2
Sequence 2, Application US/08064121
Patent No. 5641664
GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,121
FILING DATE: 24-MAY-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
FEATURE:
NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION: /note= "sequence derived from
OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
FEATURE:
NAME/KEY: -
LOCATION: 9..790
OTHER INFORMATION: /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycine
OTHER INFORMATION: phosphotransferase gene"
FEATURE:
NAME/KEY: -
LOCATION: 791..1186
OTHER INFORMATION: /label= 3'g7
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium

; OTHER INFORMATION: T-DNA gene 7"
US-08-064-121-2

Query Match 36.7%; Score 152.6; DB 1; Length 1186;
Best Local Similarity 99.3%; Pred. No. 1.4e-26;
Matches 152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgatataatcaatcagttattgaaatatttctgaatttaaaacttgc 60
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|||||

Qy 61 atcaataaawttatgttttcttggtgactataataacctgactgttattttatcaataaa 120
|||||
Db 1093 ATCAATAAATTTATGTTTCTTGGACTATATACTGACTGTGTTATTATTTATCAATAAA 1152
|||||

Qy 121 tatttaaacatattttcttcaagatgggaatt 153
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Db 1153 TATTAAACTATATTCTTCTCAAGATGGGAATT 1185
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Search completed: December 19, 2001, 17:34:14
Job time: 4291 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 16:22:38 ; Search time 2253.73 seconds
(without alignments)
95.360 Million cell updates/sec

Title: US-09-698-903b-7

Perfect score: 20
Sequence: 1 ctacggcaatgtaccagctg 20

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estfun:
2: em_esthum:
3: em_estin:
4: em_estom:
5: em_estpl:
6: em_estba:
7: em_estov:
8: em_estov:
9: em_hic:
10: gb_est1:
11: gb_est2:
12: gb_hic:
13: gb_gss:
14: em_gss_fun:
15: em_gss_hum:
16: em_gss_inv:
17: em_gss_pln:
18: em_gss_pro:
19: em_gss_rod:
20: em_gss_vrt:
21: em_gss_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	87.0	568	11	BI174209
C 2	16.8	84.0	212	10	AA090232
C 3	16.8	84.0	922	11	BC563856
C 4	16.4	82.0	700	13	AQ256131
C 5	16	80.0	170	10	AW370342
C 6	16	80.0	618	10	BE150747
C 7	15.8	79.0	325	11	BF589714
C 8	15.8	79.0	390	10	AI562674
C 9	15.8	79.0	418	11	BE857550
C 10	15.8	79.0	433	11	H66110
C 11	15.8	79.0	433	13	AQ438334
C 12	15.8	79.0	438	11	H66097

RESULT 1

BI174209/c
LOCUS

DEFINITION

OSTF013F8_1 AD-wrmCDNA Caenorhabditis elegans cDNA similar to

C46F11.2, mRNA sequence.

BI174209

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

BI174209 568 bp mRNA EST 09-JUL-2001
OSTF013F8_1 AD-wrmCDNA Caenorhabditis elegans cDNA similar to
C46F11.2, mRNA sequence.

BI174209.1 GI:14640012

EST.

Caenorhabditis elegans.

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 568)

Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,

Jackson, C., Shin-I, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,

Lee, H., Hitt, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,

Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.

Open-reading-frame sequence tags (OSTs) support the existence of at

least 17,300 genes in C. elegans

Nat. Genet. 27 (3), 332-336 (2001)

21135099

Contact: Reboul J, Vaglio P

Marc Vidal Laboratory

Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 2425

Email: Jerome.Reboul@dfci.harvard.edu

sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFsome

cloning project : Contact jerome_reboul@dfci.harvard.edu or

philippe_vaglio@dfci.harvard.edu

POLYA-No.

Location/Qualifiers

1. .568

source

ALIGNMENTS

AV632594 AV632594
BF009521 ss91h03.y
AZ215252 Sheared D
BE508621 dcl18h03.x
BG711246 p91ln.pk0
BF917369 IL3-UT011
AQ948016 Sheared D
AZ187379 SP_1009_A
AQ946406 Sheared D
BF527305 602039373
AL438079 Clone BA0
EG290991 602386981
BF311402 601896616
AW425779 58291 MAR
BB464829 BB464829
AA466153 v973g05.r
C26971 C26971 Rice
AV181598 AV181598
AI880854 atl7b03.x
AV193861 AV193861
AW048935 UI-M-BH1-
AU068795 AU068795
AI669082 wb84b08.x
AT835705 UI-M-AI0-
AA478333 zu45b04.r
AI275018 ql66h07.x
BE859284 UI-M-AI0-
AV670633 AV670633
AA124200 mg21b05.r
AW341379 x299d05.x
BB283443 BB283443
AI916284 w629a10.x
AI976324 EST270918

15.8 79.0 454 10 AV632594
15.8 79.0 472 11 BF009521
15.8 79.0 602 13 AZ215252
15.8 79.0 622 10 BE508621
15.8 79.0 681 11 BG711246
15.8 79.0 688 11 BF917369
15.8 79.0 711 13 AQ948016
15.8 79.0 712 13 AZ187379
15.8 79.0 731 13 AQ946406
15.8 79.0 923 11 BF527305
15.8 79.0 1009 13 CNS073X5
15.8 79.0 1012 11 EG290991
15.8 79.0 1700 11 BF311402
15.4 77.0 255 10 AW425779
15.4 77.0 277 10 BB464829
15.4 77.0 279 10 AA466153
15.4 77.0 299 11 C26971
15.4 77.0 300 10 AV181598
15.4 77.0 306 10 AI880854
15.4 77.0 375 10 AV193861
15.4 77.0 385 10 AW048935
15.4 77.0 408 10 AU068795
15.4 77.0 422 10 AI669082
15.4 77.0 441 10 AT835705
15.4 77.0 446 10 AA478333
15.4 77.0 447 10 AI275018
15.4 77.0 452 11 BE859284
15.4 77.0 484 10 AV670633
15.4 77.0 508 10 AA124200
15.4 77.0 509 10 AW341379
15.4 77.0 519 10 BB283443
15.4 77.0 526 10 AI916284
15.4 77.0 527 10 AI976324

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/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="AD-wrmcDNA"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauvers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
146 a 116 C 159 g 147 t
BASE COUNT
ORIGIN

```

```

Query Match      87.0%  score 17.4;  DB 11;  Length 568;
Best Local Similarity 94.7%  pred. No. 2.3e+02;
Matches 18;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
QY      1  ctacggcgaatgtaccagct 19
          ||| ||||| ||| |||||
Db      563  CTACGGCAATATACCAGCT 545

```

RESULT	2	
AA090232		
LOCUS		
DEFINITION		
ACCESSION	AA090232	212 bp mRNA
VERSION	AA090232	cdna 5', mRNA sequence.
KEYWORDS	AA090232.1	GI:1636716
SOURCE		EST.
		human.
		24-Oct-1996
		Lambda ZAP Express Homo Sapiens

ORGANISM	REFERENCE	AUTHORS	TITLE	COMMENT
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1 (bases 1 to 212)				
Liew, C.C.				
cdNAS from fetal heart (1996)				
Unpublished (1996)				
Contact: Liew CC				
Department of Laboratory Medicine and Pathobiology				
University of Toronto				
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5				
Tel: 4169788758				
Fax: 4169785650				
Email: liewccc@utcc.utoronto.ca				

PCR PRIMERS
FORWARD: 5' GCGAGCTCGAATTAACCCCTCACTAAAGG 3'
BACKWARD: 5' CCAGTGAATTGTATACGACTCACTATAGGCG 3'
Seq primer: 5' GAAATTACCCCTCACTAAAGG 3'.

Source	Location/Qualifiers
1. 212	
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_lib="Human fetal heart, Lambda ZAP Express"
	/lab_host="E. coli XL1-Blue"
	/notes="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dt adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
65 a	53 c 46 g 47 t 1 others
BASE COUNT	
GC	

```

Query Match      84.0%;   Score 16.8;   DB 10;   Length 212;
Best Local Similarity 90.0%;   Pred. No. 3.8e+02;
Matches 18;   Conservative   2;   Mismatches   2;   Indels   0;   Gaps   0;
y      1 ctacggcgaatgtaccagctg 20

```

Db	50	CTACGGCATTGTACCTGCTG	69						
RESULT	3								
BG563856									
LOCUS									
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
COMMENT									

source

BASE COUNT

243	ca	207	c	248	g	224	t
-----	----	-----	---	-----	---	-----	---

Query Match	84.0%	Score 16.8;	DB 11;	Length 922;
Best Local Similarity	90.0%;	Pred. No. 4.7e+03;		
Matches 18;	Conservative	0;	Mismatches 2;	Indels 0;
			Gaps	0;

Qy 1 ctacggcaatgtaccagctg 20
|||
Db 116 CTCCGGCAATGTACCATCTG 138

RESULT	4				
AQ256131/c					
LOCUS					
AQ256131		700 bp	DNA	GSS	23-OCT-1998
DEFINITION		nxbx0015D03r	CUGI Rice BAC Library	Oryza sativa	genomic clone
		nrbx0015D03r,	DNA sequence.		

ACCESSION	AQ256131
VERSION	AQ256131.1
KEYWORDS	GSS.
SOURCE	Oryza sativa.
ORGANISM	Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;


```

REFERENCE
AUTHORS      Ehrhartoideae; Oryzeae; Oryza.
TITLE        1. (bases 1 to 700)
JOURNAL      Wing,R.A. and Dean,R.A.
COMMENT      A BAC End Sequencing Framework to Sequence the Rice Genome
              Unpublished (1998)
              Contact: Wing RA
              Clemson University Genomics Institute
              Clemson University
              100 Jordan Hall, Clemson, SC 29634, USA
              Tel: 864 656 7288
              Fax: 864 656 4293
              Email: rwing@clemson.edu
              Seq primer: GGAACAGCTATGACCATG
              Class: BAC ends
              High quality sequence stop: 152.

FEATURES
source
1. .700
   /organism="Oryza sativa"
   /strain="Japonica"
   /cultivar="Nipponbare"
   /db_xref="taxon:4530"
   /clone="nbxb0015003r"
   /clone_lib="CUGI Rice BAC Library"
   /tissue_type="Leaf"
   /lab_host="E. coli DH10B"
   /note="Vector: pBelosBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
BASE COUNT  130 a  184 c  188 g  198 t
ORIGIN

Query Match      82.0%; Score 16.4; DB 13; Length 700;
Best Local Similarity 94.4%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3  acggcaatgtaccagctg 20
      ||||| ||||| |||||
Db  263  ACGGCAATGTCCAGCTG 246

RESULT  5
AW370342
LOCUS      AW370342      170 bp      mRNA      EST
DEFINITION RC1-BT0255-181099-012-f06 BT0255 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW370342
VERSION     AW370342.1 GI:6874996
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 170)
            HCCP http://www.ludwig.org.br/ORESTES.
REFERENCE   1
AUTHORS     The FAPESP/LICR Human Cancer Genome Project
TITLE       Unpublished (1999)
JOURNAL     Contact: Simpson A.J.G.
COMMENT

```

```

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BT0255-
181099-012-f06&t3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 170.

FEATURES
source
1. .170
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone_lib="BT0255"
   /dev_stage="Adult"
   /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT  37 a   40 c   60 g   33 t
ORIGIN

Query Match      80.0%; Score 16; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4  cggcaatgtaccagct 19
      ||||| ||||| |||||
Db  140  CGGCAATGTACCAGCT 155

RESULT  6
BE150747
LOCUS      BE150747      618 bp      mRNA      EST
DEFINITION RC1-HT0269-010300-014-h02 HT0269 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE150747
VERSION     BE150747.1 GI:8613377
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 618)
            Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC1-HT0269-010
            300-014-h02&t3=2000-03-01&t4=1)

```

Seq primer: puc 18 forward
High quality sequence start: 50
High quality sequence stop: 617.
Location/Qualifiers
1. 618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0269"
/dev_stage="Adult"
/note="Organ: head/neck; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (O.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
227 a 121 c 106 g 164 t

BASE COUNT
ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ggcaatgtaccagctg 20
|||||
Db 33 GGCAATGTACCAGCTG 48

RESULT 7
BF589714/c
LOCUS
DEFINITION naa08h06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3254267 3',
similar to TR:Q99829 Q99829 COPINE 1.; mRNA sequence.
BF589714
VERSION
KEYWORDS
SOURCE EST.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 325)
AUTHORS NCI-CGAP
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Trace considered overall poor quality
Seq primer: 400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 325

Query Match 80.0%; Score 16; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ggcaatgtaccagctg 20
|||||
Db 33 GGCAATGTACCAGCTG 48

BASE COUNT
ORIGIN

reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.
84 a 84 c 91 g 66 t

BASE COUNT
ORIGIN

Query Match 79.0%; Score 15.8; DB 11; Length 325;
Best Local Similarity 89.5%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 tacggcaatgtaccagctg 20
|||||
Db 245 TAAGGCAATGTACCAGCTG 227

RESULT 8
AI562674
LOCUS
DEFINITION TENS2662 T. cruzi epimastigote normalized cDNA Library Trypanosoma
cruzi cDNA clone 2662 5', mRNA sequence.
AI562674
ACCESSION
VERSION
KEYWORDS
SOURCE EST.
ORGANISM
Trypanosoma cruzi.
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
REFERENCE
1 (bases 1 to 390)
AUTHORS Verdun,R.E., Di Paolo,N.C., Urmenyi,T.P., Rondinelli,E., Frasch
,A.C.C. and Sanchez,D.O.
TITLE Gene discovery through expressed sequence tag sequencing in
Trypanosoma cruzi
JOURNAL Infect. Immun. 66 (11), 5393-5398 (1998)
MEDLINE 99003155
COMMENT Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
San Martin)
Av. Gral Paz entre Albarillos y Constituyentes, INTI edificio 24
CP(1650) San Martin, Prov. de BS AS, Argentina
Tel: (54-1)752-9639 or (54-1)752-0021
Fax: (54-1)752-0021 or (54-1)752-9639
Email: dsanchez@inti.gov.ar
Seq primer: T7.
Location/Qualifiers
1. 390

Query Match 79.0%; Score 15.8; DB 10; Length 390;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 tacggcaatgtaccagctg 20
|||||
Db 122 TAGCGCAAGGCACAGCTG 140

RESULT 9
BE857550/c
LOCUS
DEFINITION BE857550 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3305219 3',
similar to TR:Q99829 Q99829 COPINE 1.; mRNA sequence.
BE857550
VERSION
KEYWORDS
SOURCE EST.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 418)
AUTHORS NCI-CGAP
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Trace considered overall poor quality
Seq primer: 400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 418

Query Match 79.0%; Score 15.8; DB 10; Length 390;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 tacggcaatgtaccagctg 20
|||||
Db 122 TAGCGCAAGGCACAGCTG 140

RESULT 9
BE857550/c
LOCUS
DEFINITION BE857550 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3305219 3',
similar to TR:Q99829 Q99829 COPINE 1.; mRNA sequence.
BE857550
VERSION
KEYWORDS
SOURCE EST.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 418)
AUTHORS NCI-CGAP
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Trace considered overall poor quality
Seq primer: 400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 418

4

```
||||| | |||||
Db 326 TACGGCATTACCAGCTG 344

RESULT 14
LOCUS BF009521/c
DEFINITION ss91h03.y1 Gm-cl064 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
ACCESSION Gm-cl064-1518 5', mRNA sequence.
VERSION BF009521
KEYWORDS EST.
SOURCE BF009521.1 GI:10709797
ORGANISM soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 472)
AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, J., Cardenas, M., McCann
, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
CONTACT: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 452.
FEATURES
Location/Qualifiers
1..472
/organism="Glycine max"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl064-1518"
/clone_lib="Gm-cl064"
/tissue_type="seedling epicotyls"
/dev_stage="2 week old"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from the epicotyls of 2 week old seedling for the cultivar
Williams. The seedlings were germinated in a growth
chamber, excised above the soil level, and the plants
were placed in a 100 ppm solution of auxin for 24 hours
prior to harvesting. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT)
sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed
by XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."
BASE COUNT 136 a 88 c 103 g 145 t
ORIGIN

Query Match 79.0%; Score 15.8; DB 11; Length 472;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

||||| | |||||
Db 326 TACGGCATTACCAGCTG 344

RESULT 15
LOCUS AZ215252
DEFINITION Sheared DNA-105B6.TR Sheared DNA Trypanosoma brucei genomic clone
ACCESSION Sheared DNA-105B6, DNA sequence.
VERSION AZ215252
KEYWORDS GSS.
SOURCE AZ215252.1 GI:8432975
ORGANISM Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 602)
AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J.,
Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
Unpublished (1999)
CONTACT: Naji M. El-Sayed
Other_GSSs: Sheared DNA-105B6.TF
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through Research Genetics, Alabama, USA. Sheared DNA
end sequences search page: http://www.tigr.org/tdb/mbd/tbdb/.
Seq primer: M13-Reverse
Class: shotgun.
FEATURES
Location/Qualifiers
1..602
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-105B6"
/clone_lib="Sheared DNA"
/notes="Vector: pUC18; Site_1: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Borell, Oxford University
Press, 1999)."
BASE COUNT 143 a 153 c 150 g 156 t
ORIGIN

Query Match 79.0%; Score 15.8; DB 13; Length 602;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

||||| | |||||
Db 203 TACGGCAAGGTACGAGCTG 221

Query Match 79.0%; Score 15.8; DB 13; Length 602;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Search completed: December 19, 2001, 17:00:29
Job time: 2271 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 16:22:43 ; Search time 230.16 Seconds
(without alignments)
74.498 Million cell updates/sec

Title: us-09-698-903b-7

Perfect score: 20
Sequence: 1 ctacggcaatgtaccagctg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428562619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/NA1980.DAT.*
2: /SID88/gcgdata/geneseq/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/NA1982.DAT.*
4: /SID88/gcgdata/geneseq/NA1983.DAT.*
5: /SID88/gcgdata/geneseq/NA1984.DAT.*
6: /SID88/gcgdata/geneseq/NA1985.DAT.*
7: /SID88/gcgdata/geneseq/NA1986.DAT.*
8: /SID88/gcgdata/geneseq/NA1987.DAT.*
9: /SID88/gcgdata/geneseq/NA1988.DAT.*
10: /SID88/gcgdata/geneseq/NA1989.DAT.*
11: /SID88/gcgdata/geneseq/NA1990.DAT.*
12: /SID88/gcgdata/geneseq/NA1991.DAT.*
13: /SID88/gcgdata/geneseq/NA1992.DAT.*
14: /SID88/gcgdata/geneseq/NA1993.DAT.*
15: /SID88/gcgdata/geneseq/NA1994.DAT.*
16: /SID88/gcgdata/geneseq/NA1995.DAT.*
17: /SID88/gcgdata/geneseq/NA1996.DAT.*
18: /SID88/gcgdata/geneseq/NA1997.DAT.*
19: /SID88/gcgdata/geneseq/NA1998.DAT.*
20: /SID88/gcgdata/geneseq/NA1999.DAT.*
21: /SID88/gcgdata/geneseq/NA2000.DAT.*
22: /SID88/gcgdata/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAH25428	PCR primer for the
2	20	100.0	20	AAD06996	PCR primer MDS258
3	20	100.0	415	AAD06997	Right (5') border
4	20	100.0	416	AAD06999	Left (3') border f
5	20	100.0	1037	AAQ04705	USP-Promoter-casse
6	20	100.0	1085	AAQ04703	Legumin-signalpept
7	20	100.0	1160	AAQ04706	USP-signalpeptide
8	20	100.0	1166	AAQ04704	USP-Promoter-casse
9	20	100.0	1186	AAQ25707	Chimeric neo gene
10	20	100.0	1303	AAAT39337	Plasmid pTS88 (Eco
11	20	100.0	3153	AAZ29122	Plasmid DV131 comp

12	20	100.0	3201	12	AAQ14529	PPS029 Bt ICP codi
13	20	100.0	3201	12	AAQ15144	PVE36 Bt ICP codin
14	20	100.0	3336	21	AAZ29121	Plasmid DV130 comp
15	20	100.0	3694	21	AAZ29124	Plasmid DV133 used
16	20	100.0	3877	21	AAZ29123	Plasmid DV132 used
17	20	100.0	4832	22	AAH25423	Nucleotide sequenc
18	20	100.0	4946	18	AAH25422	T-DNA of plasmid p
19	20	100.0	4946	22	AAH25422	Nucleotide sequenc
20	20	100.0	5228	22	AAH25422	Plasmid pTS172del
21	20	100.0	5349	19	AAH25423	T-DNA of pTS24.
22	20	100.0	5864	17	AAH25423	Plasmid pTCOL13 T-
23	20	100.0	5864	17	AAH25423	Plasmid pTCOL13 T-
24	20	100.0	5865	22	AAH25423	Chimeric T-DNA of
25	20	100.0	5865	22	AAH25423	Chimeric T-DNA of
26	20	100.0	6539	21	AAH25423	E. coli plasmid pT
27	20	100.0	6548	17	AAH25423	Plasmid pTS174 use
28	20	100.0	6548	18	AAH25423	Plasmid pTS172. C
29	20	100.0	6548	21	AAH25423	E. coli plasmid pT
30	20	100.0	7492	22	AAH25423	Plasmid pTS346. U
31	20	100.0	7566	14	AAH25423	Plasmid pPS0212 co
32	20	100.0	7599	22	AAH25423	Nucleotide sequenc
33	20	100.0	7639	14	AAH25423	Plasmid pJD884 con
34	20	100.0	24593	6	AAH25423	Sequence of opine
35	20	100.0	24596	6	AAH25423	Complete nucleotid
36	19	95.0	19	20	AAH25423	Transformed Arabid
37	18.4	92.0	1077	22	AAH25423	Right flanking reg
38	18	90.0	21	22	AAH25423	T-DNA right border
39	18	90.0	22	22	AAH25423	PCR primer for the
40	18	90.0	22	22	AAH25423	PCR primer MDS193
41	17	85.0	20	21	AAH25423	p302 EcoRI primer
42	15.8	79.0	309	21	AAH25423	Human 5' EST Isola
43	15.8	79.0	1290	21	AAH25423	Nucleotide sequenc
44	15.8	79.0	4828	22	AAH25423	Human cDNA sequenc
45	15.4	77.0	11871	20	AAH25423	Enterococcus faeca

ALIGNMENTS

RESULT 1
AAH25428
ID AAH25428 standard; DNA; 20 BP.
XX
AC AAH25428;
XX
XX 22-AUG-2001 (first entry)
XX
XX PCR primer for the right border in transgenic plant MS-BN1.
DE
XX Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene;
KW fertility restorer gene; barnase gene; PCR primer; ss.
KW
XX Synthetic.
OS
XX
XX WO200141558-A1.
XX
XX 14-JUN-2001.
XX
XX 06-DEC-2000; 2000WO-EPI2872.
XX
XX 08-DEC-1999; 99US-0457037.
XX
XX (AVET) AVENTIS CROPS SCIENCE NV.
XX
XX De Both G, De Beuckeleer M;
XX
XX Left (3') border f
XX
XX USP-Promoter-casse
XX Legumin-signalpept
XX
XX USP-signalpeptide
XX
XX USP-Promoter-casse
XX Chimeric neo gene
XX Plasmid pTS88 (Eco
XX Plasmid DV131 comp
PS

Transgenic winter oilseed rape plants suited for producing hybrid seed
with improved qualities, comprises a male-sterility gene and fertility
restorer gene, integrated into the genome -
Example 4; Page 43; 98pp; English.

XX CC The specification describes a pair of transgenic winter oilseed rape
 CC plants suited for producing hybrid seed. One of the plants has an
 CC expression cassette comprising a male-sterility gene (e.g. barnase
 CC gene), and the other plant has an expression cassette comprising a
 CC fertility restorer gene (e.g. barstar gene), integrated into the genome.
 CC The fertility restorer gene is capable of preventing the activity of the
 CC male-sterility gene. The plant pair is useful for producing hybrid seed.
 CC Plants developed from the hybrid seed have agronomic performance,
 CC genetic stability and adaptability to different genetic backgrounds.
 CC PCR primers AAB25427-28 were used to amplify the right border of
 CC a vector in a transgenic plant which carries the TA29-barnase
 CC transgene.

XX SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;

XX CC Query Match 100.0%; Score 20; DB 22; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 0.26;
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctacggcaatgtaccagctg 20
 |||||
 Db 1 ctacggcaatgtaccagctg 20

RESULT 2
 AAD06996
 ID AAD06996 standard; DNA; 20 BP.
 AC AAD06996;
 XX
 DT 06-AUG-2001 (first entry)
 XX
 DE PCR primer MDB258 to generate the flanking region of elite event MS-B2.
 XX
 DE MS-B2 elite event; transgenic Brassica plant; transformation event;
 KW male-sterility gene; PCR primer; thermal asymmetric interlaced;
 KW TAIL; ss.
 XX
 OS Agrobacterium sp.
 XX
 PN WO200131042-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-EP10680.
 XX
 PR 29-OCT-1999; 99US-0430497.
 XX
 PA (AVET) AVENTIS CROPS SCIENCE NV.
 XX
 PI Weston B, De Beuckeleer M;
 XX
 DR WPI; 2001-300517/31.
 XX
 PT Transgenic Brassica plants, seeds, cells or tissues, characterized by
 PT harboring specific transformation events, particularly by presence of
 PT male-sterility gene, at specific location in its genome -
 XX
 PS Example 3; Page 28; 53pp; English.
 XX
 CC The present invention relates to a transgenic Brassica plant or its
 CC seed, cells or tissues, characterised by harbouring a specific
 CC transformation event, particularly by the presence of a male-sterility
 CC gene, at a specific location in the Brassica genome. Transgenic
 CC Brassica plant is useful for producing a hybrid seed by crossing the
 CC transgenic plant with a male-fertile Brassica plant and harvesting the
 CC hybrid seed from the transgenic Brassica plant.
 CC The present sequence is tertiary thermal interlaced (TAIL)-PCR primer
 CC MDB258 used to right (5') and left (3') border flanking region of elite
 CC event MS-B2. This primer corresponds to position 224-243 of plasmid
 CC pTColl13.

XX SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;

XX CC Query Match 100.0%; Score 20; DB 22; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 0.26;
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctacggcaatgtaccagctg 20
 |||||
 Db 1 ctacggcaatgtaccagctg 20

RESULT 3
 AAD06997/c
 ID AAD06997 standard; DNA; 415 BP.
 AC AAD06997;
 XX
 DT 06-AUG-2001 (first entry)
 XX
 DE Right (5') border flanking region of elite event MS-B2.
 XX
 DE MS-B2 elite event; transgenic Brassica plant; transformation event;
 KW male-sterility gene; ds.
 XX
 OS Chimeric - Agrobacterium sp.
 OS Chimeric - Brassica sp.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..234
 FT /tag= a
 FT /note= "Corresponds to plant DNA"
 FT misc_feature 235..415
 FT /tag= b
 FT /note= "Corresponds to T-DNA"
 XX
 PN WO200131042-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-EP10680.
 XX
 PR 29-OCT-1999; 99US-0430497.
 XX
 PA (AVET) AVENTIS CROPS SCIENCE NV.
 XX
 PI Weston B, De Beuckeleer M;
 XX
 DR WPI; 2001-300517/31.
 XX
 PT Transgenic Brassica plants, seeds, cells or tissues, characterized by
 PT harboring specific transformation events, particularly by presence of
 PT male-sterility gene, at specific location in its genome -
 XX
 PS Claim 11; Page 51; 53pp; English.
 XX
 CC The present invention relates to a transgenic Brassica plant or its
 CC seed, cells or tissues, characterised by harbouring a specific
 CC transformation event, particularly by the presence of a male-sterility
 CC gene, at a specific location in the Brassica genome. Transgenic
 CC Brassica plant is useful for producing a hybrid seed by crossing the
 CC transgenic plant with a male-fertile Brassica plant and harvesting the
 CC hybrid seed from the transgenic Brassica plant.
 CC The present sequence is right (5') border flanking region of elite event
 CC MS-B2.
 XX
 SQ Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;

XX CC Query Match 100.0%; Score 20; DB 22; Length 415;
 CC Best Local Similarity 100.0%; Pred. No. 0.38;
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

QY 1 ctacggcaatgtaccagctg 20
   |||||
Db 415 CTACGGCAATGTACCAGCTG 396

RESULT 4
AAD06999
ID AAD06999 standard; DNA; 416 BP.
XX AC AAD06999;
XX DT 06-AUG-2001 (first entry)
XX DE Left (3') border flanking region of elite event MS-B2.
XX KW MS-B2 elite event; transgenic Brassica plant; transformation event;
XX KW male-sterility gene; ds.
XX OS Chimeric - Agrobacterium sp.
XX OS Chimeric - Brassica sp.
XX FH Key Location/Qualifiers
FT misc_feature 1..193
FT /*tag= a
FT /note= "Corresponds to T-DNA"
FT misc_feature 194..416
FT /*tag= b
FT /note= "Corresponds to plant DNA"
XX WO200131042-A2.
XX 03-MAY-2001.
XX 26-OCT-2000; 2000WO-EP10680.
XX 29-OCT-1999; 99US-0430497.
XX (AVET ) AVENTIS CROPS SCIENCE NV.
XX Weston B, De Beuckeleer M;
XX WPI; 2001-300517/31.
XX Transgenic Brassica plants, seeds, cells or tissues, characterized by
XX harboring specific transformation events, particularly by presence of
XX male-sterility gene, at specific location in its genome -
XX Claim 11; Page 52; 53pp; English.
XX The present invention relates to a transgenic Brassica plant or its
XX seed, cells or tissues, characterised by harbouring a specific
XX transformation event, particularly by the presence of a male-sterility
XX gene, at a specific location in the Brassica genome. Transgenic
XX Brassica plant is useful for producing a hybrid seed by crossing the
XX transgenic plant with a male-fertile Brassica plant and harvesting the
XX hybrid seed from the transgenic Brassica plant.
XX The present sequence is left (3') border flanking region of elite event
XX MS-B2.
XX Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;

Query Match 100.0%; Score 20; DB 22; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
   |||||
Db 1 ctacggcaatgtaccagctg 20

RESULT 5

```

```

AAQ04705
ID AAQ04705 standard; DNA; 1037 BP.
XX AC AAQ04705;
XX DT 12-OCT-1990 (first entry)
XX DE USP-Promoter-cassette USP-Pr.T7.1.
XX KW Foreign DNA incorporation; recombinant DNA techniques;
XX KW higher plant genome; legumin; USP-Pr.T7-1; ss.
XX PN DE3920034-A.
XX 31-MAY-1990.
XX 20-JUN-1989; 89DE-3920034.
XX 19-SEP-1988; 88DD-0319887.
XX (PFLA-) VE KOMB PFLANZENZUC.
XX Bassuner R, Baumlein H, Muntz K, Hai NV, Wobus U;
XX WPI; 1990-172459/23.
XX Incorporation of DNA into higher plant genome - by specified
XX recombinant DNA techniques.
XX Disclosure; ; pp; German.
XX The unique BglII-Ort (720-725) site is for ligating foreign DNA and the
XX HindIII-Ort in the 3' polylinker (1032-1037) for cloning the
XX cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
XX transfected.
XX See also AAQ04703-Q04706.
XX Sequence 1037 BP; 338 A; 174 C; 166 G; 359 T; 0 other;

Query Match 100.0%; Score 20; DB 11; Length 1037;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
   |||||
Db 841 ctacggcaatgtaccagctg 860

RESULT 6
AAQ04703
ID AAQ04703 standard; DNA; 1085 BP.
XX AC AAQ04703;
XX DT 12-OCT-1990 (first entry)
XX DE Legumin-signalpeptide cassette Le-Sig.T7.
XX KW Foreign DNA incorporation; recombinant DNA techniques;
XX KW higher plant genome; legumin; B4 gene; signalpeptide; Le-Sig.T7.; ss.
XX FH Key Location/Qualifiers
FT CDS 747..814
FT /*tag= a
FT /product=Legumin-signalpeptide
XX DE3920034-A.
XX 31-MAY-1990.
XX 20-JUN-1989; 89DE-3920034.
XX

```

```

PR 19-SEP-1988; 88DD-0319887.
XX (PFLA-) VE KOMB PFLANZENZUC.
XX Bassuner R, Baumlein H, Muntz K, Hai NV, Wobus U;
XX WPI; 1990-172459/23.
XX P-PSDB; AAR05198.
XX
XX Incorporation of DNA into higher plant genome - by specified
XX recombinant DNA techniques.
XX Disclosure; ; pp: German.
XX
XX The Legumin gene B4 is used. The unique BglII-Ort (815-820) site is for
XX ligating foreign DNA and the HindIII-Ort in the 3' polylinker
XX (1080-1085) for cloning the cassette in the Ti-vector pGA471.
XX The cassette is cloned into the binary Ti-vectors pGA471 and
XX Agrobacterium tumefaciens is transfected.
XX See also AAQ04703-Q04706.
XX
XX Sequence 1085 BP; 368 A; 219 C; 155 G; 343 T; 0 other;

Query Match 100.0%; Score 20; DB 11; Length 1085;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
Db 889 ctacggcaatgtaccagctg 908
|||||

RESULT 7
AAQ04706
ID AAQ04706 standard; DNA; 1160 BP.
XX
XX AAQ04706;
XX
XX 12-OCT-1990 (first entry)
XX USP-signalpeptide cassette USP-Sig.T7.
XX Foreign DNA incorporation; recombinant DNA techniques;
XX higher plant genome; signalpeptide; USP-Sig.T7.; ss.
XX
XX Key Location/Qualifiers
XX CDS 708..877
XX /*tag= a
XX /product=signalpeptide
XX 747..817
XX Intron
XX
XX DE3920034-A.
XX
XX 31-MAY-1990.
XX
XX 20-JUN-1989; 89DE-3920034.
XX
XX 19-SEP-1988; 88DD-0319887.
XX (PFLA-) VE KOMB PFLANZENZUC.
XX Bassuner R, Baumlein H, Muntz K, Hai NV, Wobus U;
XX WPI; 1990-172459/23.
XX P-PSDB; AAR05199.
XX
XX Incorporation of DNA into higher plant genome - by specified
XX recombinant DNA techniques.
XX Disclosure; ; pp: German.
XX
XX The unique BglII-Ort (890-895) site is for

```

```

CC ligating foreign DNA and the HindIII-Ort in the 3' polylinker
CC (1155-1160) for cloning the cassette in the Ti-vector pGA471.
CC The cassette is cloned into the binary Ti-vectors pGA471 and
CC Agrobacterium tumefaciens is transfected.
CC See also AAQ04703-Q04706.
XX
XX Sequence 1160 BP; 369 A; 192 C; 188 G; 411 T; 0 other;

Query Match 100.0%; Score 20; DB 11; Length 1160;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
Db 964 ctacggcaatgtaccagctg 983
|||||

RESULT 8
AAQ04704
ID AAQ04704 standard; DNA; 1166 BP.
XX
XX AAQ04704;
XX
XX 12-OCT-1990 (first entry)
XX USP-Promoter-cassette USP-Pr.T7.2.
XX Foreign DNA incorporation; recombinant DNA techniques;
XX higher plant genome; legumin; USP-Pr.T7-2; ss.
XX
XX DE3920034-A.
XX
XX 31-MAY-1990.
XX
XX 20-JUN-1989; 89DE-3920034.
XX
XX 19-SEP-1988; 88DD-0319887.
XX (PFLA-) VE KOMB PFLANZENZUC.
XX Bassuner R, Baumlein H, Muntz K, Hai NV, Wobus U;
XX WPI; 1990-172459/23.
XX Incorporation of DNA into higher plant genome - by specified
XX recombinant DNA techniques.
XX Disclosure; ; pp: German.
XX
XX The unique BglII-Ort (720-725) site is for ligating foreign DNA and the
XX HindIII-Ort in the 3' polylinker (1261-1266) for cloning the
XX cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
XX transfected.
XX See also AAQ04703-Q04706.
XX
XX Sequence 1166 BP; 381 A; 208 C; 196 G; 381 T; 0 other;

Query Match 100.0%; Score 20; DB 11; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
Db 1070 ctacggcaatgtaccagctg 1089
|||||

RESULT 9
AAQ25707
ID AAQ25707 standard; DNA; 1186 BP.
XX
XX AAQ25707;

```

```

XX 07-DEC-1992 (first entry)
XX Chimeric neo gene probe.
XX Nicotiana tabacum; neomycine phosphotransferase; Agrobacterium; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX promoter 1..8
XX CDS 9..790
XX misc_feature 791..1186
XX /tag= a
XX /note= "sequence derived from tapetum specific
XX promoter of Nicotiana tabacum"
XX 9..790
XX /tag= b
XX /product= neomycine_phosphotransferase
XX 791..1186
XX /tag= c
XX /note= "3' regulatory sequence contg. the
XX polyadenylation site derived from
XX Agrobacterium T-DNA gene 7"
XX
XX WO9209696-A.
XX 11-JUN-1992.
XX 21-NOV-1991; 91WO-EP02198.
XX 23-NOV-1990; 90EP-0403332.
XX 08-JUL-1991; 91EP-0401888.
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX Dhalluin K, Goebel E;
XX WPI; 1992-217075/26.
XX Transforming monocotyledonous plants e.g. cereals - comprises
XX wounding and/or degrading cells of intact plant tissue or
XX embryogenic callus
XX Disclosure; Page 60; 76pp; English.
XX Two transformed corn plants were analysed by means of Southern
XX hybridisation. As a probe, a 1184 bp EcoRI-HindIII fragment derived
XX from another plasmid was used. The sequence of that plasmid is
XX given below. Results showed that at least a chimeric neo gene was
XX integrated into the plant genomic DNA.
XX Sequence 1186 BP; 244 A; 317 C; 325 G; 300 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 13; Length 1186;
XX Best Local Similarity 100.0%; Pred. No. 0.44;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ctacggcaatgtaccagctg 20
XX | | | | | | | | | | | | | | | |
XX Db 1033 ctacggcaatgtaccagctg 1052
XX
XX RESULT 10
XX AAT39337
XX ID AAT39337 standard; DNA; 1303 BP.
XX AC AAT39337;
XX
XX 22-JAN-1997 (first entry)
XX Plasmid pTS88 (EcoRI-HindIII fragment).
XX Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;

```

```

KW transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds.
XX Synthetic.
XX Key Location/Qualifiers
XX misc_feature 1..35
XX /tag= a
XX /label= pGEM2
XX /note= "polylinker of pGEM2"
XX promoter 36..694
XX /tag= b
XX /label= p35S
XX /function= 35S promoter of cauliflower mosaic virus
XX strain CM1841
XX CDS 695..967
XX /tag= c
XX /label= barstar
XX /product= Bacillus amyloliquefaciens barstar
XX 968..1287
XX /tag= d
XX /label= 3'g7
XX /function= region containing polyadenylation signal
XX of gene 7 og Agrobacterium T-DNA
XX misc_feature 1288..1303
XX /tag= e
XX /label= pGEM2
XX /note= "polylinker of pGEM2"
XX WO9626283-A1.
XX 29-AUG-1996.
XX 21-FEB-1996; 96WO-EP00722.
XX 21-FEB-1995; 95EP-0400364.
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX Botterman J, Cornelissen M, Michiels F;
XX WPI; 1996-402373/40.
XX Prodn. of male sterile plants by transforming with a chimaeric
XX construct - comprising a male sterility DNA e.g. barnase and a
XX co-regulating gene, e.g. barstar, into the nuclear genome, useful
XX for generating hybrid cultivars
XX Example 1; Page 38; 56pp; English.
XX The HindIII-EcoRI fragment (AAT39337) of plasmid pTS88 contains
XX barstar DNA under control of a 35S promoter. The plasmid was
XX used with pTS174 (see also AAT39336) contg. barnase DNA under
XX control of the stamen-specific promoter EI to produce male sterile
XX rice cv. Kochihibiki transgenic plants, and with plasmid pV8136
XX (see also AAT39338) contg. barnase DNA under control of the stamen-
XX specific PCA55 promoter to produce male sterile maize plants.
XX Expression of barnase (a ribonuclease) in the stamen leads to male
XX sterility. Constitutive expression of barstar counteracts possible
XX low level expression of barnase DNA in non-stamen tissue.
XX Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 17; Length 1303;
XX Best Local Similarity 100.0%; Pred. No. 0.44;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ctacggcaatgtaccagctg 20
XX | | | | | | | | | | | | | | | |
XX Db 1098 ctacggcaatgtaccagctg 1117
XX
XX RESULT 11

```

DT 27-JAN-1

DR WPI; 1991-339820/46.
 XX Modified *Bacillus thuringiensis* insecticidal crystal protein
 PT genes - having A and T sequences changed to G and C sequences
 PT encoding same amino acids, for increased expression levels
 XX
 PS Disclosure; Fig 6(c); 78pp; English.
 XX
 CC "n" in the sequence refers to not known nucleotides.
 CC pPS029 (AAQ14529) is identical to pVE36, but carries both the amino-
 CC terminal modification and the internal modification of the Bt ICP
 CC coding sequence.
 CC See also AAQ14529, AAQ15142-44.
 XX
 SQ Sequence 3201 BP; 915 A; 651 C; 700 G; 930 T; 5 other;
 Query Match 100.0%; Score 20; DB 12; Length 3201;
 Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 QY 1 ctacggcaatgtaccagctg 20
 |||||
 Db 3025 ctacggcaatgtaccagctg 3044
 RESULT 14
 AAZ29121
 ID AAZ29121 standard; DNA; 3336 BP.
 XX
 AC AAZ29121;
 XX
 DT 21-FEB-2000 (first entry)
 XX
 DE Plasmid DV130 comprising L3/MGFP:NPTII/Tr7 expression cassette.
 XX
 KW Transgenic seed; marker; aleurone-specific promoter; Plasmid DV130;
 KW GFP:NPTII fusion protein construct; L3/MGFP:NPTII/Tr7; maize R gene;
 KW expression cassette; maize L3 oleosin gene; chimeric gene; transgene;
 KW MGFP:NPTII translational fusion; Tr7 terminator; luciferase gene;
 KW Green fluorescent protein; GFP; gene fusion; selection; screening;
 KW transformant; expression; automated seed screening technique; assay;
 KW screenable marker; embryogenic tissue; implementation; ds.
 XX
 OS Synthetic.
 XX
 PN WO9960129-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 18-MAY-1999; 99WO-US11023.
 XX
 PR 18-MAY-1998; 98US-0080625.
 XX
 PA (DEKA-) DEKALB GENETICS CORP.
 XX
 PI Kriz AL, Spencer TM;
 XX
 PS WPI; 2000-072441/06.
 XX
 XX Screenable marker genes useful for identification of transgenic seeds
 PT for plant breeding -
 XX
 PS Example 1; Page 163-164; 182pp; English.
 XX
 CC The present DNA sequence is the plasmid DV130, that is used in the
 CC generation of GFP:NPTII fusion protein constructs. It contains an
 CC expression cassette comprising, a promoter from the maize L3 oleosin
 CC gene, the coding sequence of MGFP:NPTII translational fusion, excised
 CC from DV127 and the Tr7 terminator. This plasmid is used to carry a
 CC chimeric gene, comprising an aleurone-specific promoter like L3, that is
 CC operably linked to a gene encoding a screenable marker, like Green
 CC fluorescent protein (GFP), luciferase or maize R gene. The gene fusions

CC allow both selection and screening of transformants. The aleurone-
 CC specific promoters direct the expression of the marker genes in
 CC embryogenic tissues, allowing selection and screening of viable
 CC transgenic seeds. Screening of transgenic seeds avoids the need for
 CC growing and assaying of seeds for transgenes and allows implementation
 CC of automated seed screening techniques for the identification of
 CC transgenic seeds.
 XX
 SQ Sequence 3336 BP; 888 A; 830 C; 764 G; 854 T; 0 other;
 Query Match 100.0%; Score 20; DB 21; Length 3336;
 Best Local Similarity 100.0%; Pred. No. 0.5; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 QY 1 ctacggcaatgtaccagctg 20
 |||||
 Db 2862 ctacggcaatgtaccagctg 2881
 RESULT 15
 AAZ29124
 ID AAZ29124 standard; DNA; 3694 BP.
 XX
 AC AAZ29124;
 XX
 DT 21-FEB-2000 (first entry)
 XX
 DE Plasmid DV133 used for construction of GFP:NPTII fusion protein.
 XX
 KW Transgenic seed; marker; aleurone-specific promoter; Plasmid DV133;
 KW GFP:NPTII fusion protein construct; L3/rACT1 intron/EGFP:NPTII/Tr7;
 KW expression cassette; maize L3 oleosin gene; chimeric gene; transgene;
 KW EGFP:NPTII translational fusion; Tr7 terminator; luciferase gene;
 KW Green fluorescent protein; GFP; gene fusion; maize R gene; selection;
 KW screenable marker; screening; automated seed screening technique; assay;
 KW transformant; expression; embryogenic tissue; implementation; ds.
 XX
 OS Synthetic.
 XX
 PN WO9960129-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 18-MAY-1999; 99WO-US11023.
 XX
 PR 18-MAY-1998; 98US-0080625.
 XX
 PA (DEKA-) DEKALB GENETICS CORP.
 XX
 PI Kriz AL, Spencer TM;
 XX
 PS WPI; 2000-072441/06.
 XX
 XX Screenable marker genes useful for identification of transgenic seeds
 PT for plant breeding -
 XX
 PS Example 1; Page 168-170; 182pp; English.
 XX
 CC The present DNA sequence is the plasmid DV133, comprising
 CC L3/rACT1 intron/EGFP:NPTII/Tr7, that is used in the generation of
 CC GFP:NPTII fusion protein constructs. It contains an expression cassette
 CC comprising, a promoter from the maize L3 oleosin gene, the rice actin 1
 CC intron, the coding sequence of EGFP:NPTII translational fusion, excised
 CC from DV126 and the Tr7 terminator. This plasmid is used to carry a
 CC chimeric gene, comprising an aleurone-specific promoter like L3, that is
 CC operably linked to a gene encoding a screenable marker, like Green
 CC fluorescent protein (GFP), luciferase or maize R gene. The gene fusions
 CC allow both selection and screening of transformants. The aleurone-
 CC specific promoters direct the expression of the marker genes in
 CC embryogenic tissues, allowing selection and screening of viable
 CC transgenic seeds. Screening of transgenic seeds avoids the need for
 CC growing and assaying of seeds for transgenes and allows implementation

CC of automated seed screening techniques for the identification of
 CC transgenic seeds.

XX
 SQ Sequence 3694 BP; 890 A; 984 C; 914 G; 906 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3694;
 Best Local Similarity 100.0%; Pred. NO. 0.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
 |||||
 Db 3220 ctacggcaatgtaccagctg 3239

Search completed: December 19, 2001, 17:31:51
 Job time: 4148 sec

GenCore version 4.5
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EM nucleic - nucleic search, using sw model

Run 00: December 19, 2001, 16:22:38 ; Search time 1631.12 Seconds
(without alignments)
202.280 Million cell updates/sec

Title: US-09-698-903B-7

Perfect score: 20
Sequence: 1 ctacggcaatgtaccagctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**

2: gb_htg:**

3: gb_in:**

4: gb_om:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pl:**

9: gb_pr:**

10: gb_ro:**

11: gb_sts:**

12: gb_sy:**

13: gb_un:**

14: gb_vi:**

15: em_ba:**

16: em_fun:**

17: em_hum:**

18: em_in:**

19: em_om:**

20: em_or:**

21: em_ov:**

22: em_pat:**

23: em_ph:**

24: em_pl:**

25: em_ro:**

26: em_sts:**

27: em_sy:**

28: em_un:**

29: em_vi:**

30: em_htgo_hum:**

31: em_htgo_inv:**

32: em_htgo_rod:**

33: em_htg_hum:**

34: em_htg_inv:**

35: em_htg_rod:**

36: em_htg_other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX127754 Sequence
2	20	100.0	20	6	AX172448 Sequence
3	20	100.0	249	12	X05579 Soybean bet
c	4	20	100.0	415	6 AX127755 Sequence
5	20	100.0	416	6	AX127757 Sequence
6	20	100.0	831	1	ATTRN7
7	20	100.0	878	1	ATTDNA
8	20	100.0	1037	6	A10942
9	20	100.0	1083	6	A10939
10	20	100.0	1160	6	A10943
11	20	100.0	1166	6	A10941
12	20	100.0	1186	6	A18051
13	20	100.0	1186	6	AR095107
14	20	100.0	1186	6	AR098313
15	20	100.0	1186	6	AX012338
16	20	100.0	1186	6	I49886 Sequence 2
17	20	100.0	1186	6	I82374 Sequence 2
c	18	20	100.0	2476	12 TBI251013
19	20	100.0	3200	6	I44104
20	20	100.0	3201	6	I44103
c	21	20	100.0	3236	12 TBI251014
22	20	100.0	4832	6	AX172441
c	23	20	100.0	4946	6 A60108
c	24	20	100.0	4946	6 A76915
c	25	20	100.0	4946	6 AR098307
c	26	20	100.0	4946	6 AX172440
c	27	20	100.0	5349	6 A71437
c	28	20	100.0	5560	6 A60112
c	29	20	100.0	5560	6 AR098311
c	30	20	100.0	5865	6 AX127748
c	31	20	100.0	5865	6 AX127748
32	20	100.0	6539	6	E31991
33	20	100.0	6548	6	A60109
34	20	100.0	6548	6	A76916
35	20	100.0	6548	6	AR098308
36	20	100.0	6548	6	E31990
37	20	100.0	7566	6	A24783
38	20	100.0	7566	6	AR074388
39	20	100.0	7599	6	AX063413
40	20	100.0	7639	6	A24782
41	20	100.0	7639	6	AR074387
c	42	20	100.0	7811	6 AR078675
c	43	20	100.0	12095	12 BINHYGDNA
c	44	20	100.0	24595	1 ATACH5
c	45	20	100.0	24595	6 E00404

ALIGNMENTS

RESULT 1	AX127754	Sequence 7	20 bp	DNA	PAT	15-MAY-2001
LOCUS	AX127754	Sequence 7	from Patent	WO0131042.		
DEFINITION	AX127754					
ACCESSION	AX127754.1	GI:14134401				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
1..20						
/organism="synthetic construct"						
/db_xref="taxon:32630"						
/note="primer M8258"						

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BASE COUNT      5 a      6 c      5 g      4 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 1 CTACGGCAATGTACCAGCTG 20

RESULT 2
AX172448
LOCUS AX172448 20 bp DNA PAT 03-JUL-2001
DEFINITION Sequence 9 from Patent WO0141558.
ACCESSION AX172448
VERSION AX172448.1 GI:14597560
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 20)
AUTHORS de Both.G. and de Beuckeleer,M.
TITLE Hybrid winter oilseed rape and methods for producing same
JOURNAL Patent: WO 0141558-A 9 14-JUN-2001;
Aventis CropScience N.V. (BE)
FEATURES
source
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer 258"
BASE COUNT      5 a      6 c      5 g      4 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 1 CTACGGCAATGTACCAGCTG 20

RESULT 3
ARGMTUB
LOCUS ARGMTUB 249 bp DNA SYN 02-APR-1988
DEFINITION Soybean beta-1-tubulin gene fused to T1 plasmid unit 7 3UTR.
ACCESSION X05579
VERSION X05579.1 GI:58087
KEYWORDS beta-tubulin; fusion gene; plasmid.
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 249)
AUTHORS Guiltinan,M.J., Velten,J., Bustos,M.M., Cyr,R.J., Schell,J. and
Fosket,D.E.
TITLE The expression of a chimeric soybean beta-tubulin gene in tobacco
JOURNAL Mol. Gen. Genet. 207, 328-334 (1987)
FEATURES
source
1..249
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
1..51
/note="fusion product (17AA); Protein sequence is in
conflict with the conceptual translation"
/codon_start=1
/transl_table=11
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/db_xref="GI:4376141"
/translation="AMAAWASSNWSTDPFMS"
CDS
1..51
/note="fusion product (17AA); Protein sequence is in
conflict with the conceptual translation"
/codon_start=1
/transl_table=11
/protein_id="CAA29084.1"
/db_xref="GI:4376141"
/translation="AMAAWASSNWSTDPFMS"

misc_feature 1..13
/note="beta-1-tubulin sequence"
14..28
/note="pUC 13 polylinker"
29..35
/note="Sal I linker"
37
/note="theroretical fusion junction (24) with gene 7 of T1
plasmid"
173..178
/note="put.polyA signal"
198
/note="polyA site"
220..225
/note="polyA site"
BASE COUNT 76 a 47 c 38 g 88 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 12; Length 249;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 110 CTACGGCAATGTACCAGCTG 129

RESULT 4
AX127755/c
LOCUS AX127755 415 bp DNA PAT 15-MAY-2001
DEFINITION Sequence 8 from Patent WO0131042.
ACCESSION AX127755
VERSION AX127755.1 GI:14134402
KEYWORDS
SOURCE
synthetic construct.
synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 415)
AUTHORS Weston,B. and de Beuckeleer,M.
TITLE Male-sterile brassica plants and methods for producing same
JOURNAL Patent: WO 0131042-A 8 03-MAY-2001;
Aventis CropScience N.V. (BE)
FEATURES
source
1..415
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' border flanking region of elite event MS-B2"
1..234
/note="plant DNA"
235..415
/note="T-DNA"
BASE COUNT 154 a 55 c 70 g 136 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 415;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 415 CTACGGCAATGTACCAGCTG 396

RESULT 5
AX127757
LOCUS AX127757 416 bp DNA PAT 15-MAY-2001
DEFINITION Sequence 10 from Patent WO0131042.
ACCESSION AX127757
VERSION AX127757.1 GI:14134404
KEYWORDS
SOURCE
synthetic construct.

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ORGANISM    synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 416)
AUTHORS    Weston,B. and de Beuckeleer,M.
TITLE      Male-sterile brassica plants and methods for producing same
JOURNAL    Patent: WO 0131042-A 10 03-MAY-2001;
            Aventis CropScience N.V. (BE)
FEATURES   Location/Qualifiers
            source             1..416
                                /organism="synthetic construct"
                                /db_xref="taxon:32630"
                                /notes="3' border flanking region of elite event MS-B2"
            misc_feature      1..193
                                /note="T-DNA"
            misc_feature      194..416
                                /note="plant DNA"
BASE COUNT  137 a   72 c   54 g   152 t   1 others
ORIGIN
            1 ctacggcaatgtaccagctg 20
            ||||||||||||||||||
            1 CTACGGCAATGTACCAGCTG 20

Query Match      100.0%; Score 20; DB 6; Length 416;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
    ||||||||||||||||||
DB 1 CTACGGCAATGTACCAGCTG 20

RESULT 6
LOCUS      ATNRN7      831 bp      DNA      BCT      02-SEP-1999
DEFINITION Agrobacterium tumefaciens gene encoding 'transcript 7' mRNA for a
            protein with unknown function.
ACCESSION  V00090
VERSION    V00090.1 GI:39180
KEYWORDS   unidentified reading frame.
SOURCE     Agrobacterium tumefaciens.
ORGANISM   Agrobacterium tumefaciens.
            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
            Rhizobiaceae; Rhizobium.
REFERENCE   1 (bases 1 to 831)
AUTHORS    Dhaese,P.; De Greve,H.; Gielen,J.; Seurinck,J.; Van Montagu,M.M.
            and Schell,J.
TITLE      Identification of sequences involved in the polyadenylation of
            higher plant nuclear transcripts using Agrobacterium T-DNA genes as
            models
JOURNAL    EMBO J. 2, 419-426 (1983)
REFERENCE   2 (bases 76 to 100)
AUTHORS    Dhaese,P.
TITLE      Direct Submission
COMMENT    Submitted (27-MAY-1983) to the EMBL/GenBank/DBJ databases
          Data kindly reviewed (27-MAY-1983) by Dhaese P.
FEATURES   Location/Qualifiers
            source             1..831
                                /organism="Agrobacterium tumefaciens"
                                /strain="(octopine T-DNA)"
                                /db_xref="taxon:358"
            old_sequence      75..81
                                /note="CG [1] revised CCAGAGG [2]"
                                /citation=[1]
                                /citation=[2]
            old_sequence      99..101
                                /note="CCA [1] revised CTA [2]"
                                /citation=[1]
                                /citation=[2]
            mRNA              132..673
                                /note="transcript 7 (alternate)"
            mRNA              132..672
                                /note="transcript 7"
            CDS                148..528
                                /note="unknown gene (148 is 1st base in codon) (525 is 3rd
                                base in codon)"

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/codon_start=1
/transl_table=11
/protein_id="CAA23429.1"
/db_xref="GI:39181"
/db_xref="SWISS-PROT:P03867"
/translation="MNFADTPTLASLDLDWACEEFIKTYGASPOLETGEVQTNNGLLY
LYKGSLSQRIHDTHLKFEKEELSFTTIKPAEMKAQSDITYVAIFQSNYFLCVSN
PEKGFRLCHNRPFPLYPIVAHGSMS"
BASE COUNT  262 a   176 c   138 g   255 t
ORIGIN
            1 ctacggcaatgtaccagctg 20
            ||||||||||||||||||
            584 CTACGGCAATGTACCAGCTG 603

Query Match      100.0%; Score 20; DB 1; Length 831;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
    ||||||||||||||||||
DB 584 CTACGGCAATGTACCAGCTG 603

RESULT 7
LOCUS      ATTDNA      878 bp      DNA      BCT      25-MAR-1996
DEFINITION Agrobacterium tumefaciens crown gall tumor T-DNA from T1 (tumor
            inducing) plasmid pTiA6.
ACCESSION  X00431
VERSION    X00431.1 GI:39150
KEYWORDS   plasmid.
SOURCE     Agrobacterium tumefaciens.
            Agrobacterium tumefaciens.
            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
            Rhizobiaceae; Rhizobium.
REFERENCE   1 (bases 1 to 878)
AUTHORS    McPherson,J.C.
TITLE      DNA sequence analysis of crown gall tumor T-DNA encoding the 0.7 kb
            transcript
JOURNAL    Nucleic Acids Res. 12 (5), 2317-2325 (1984)
MEDLINE    84169535
FEATURES   Location/Qualifiers
            source             1..878
                                /organism="Agrobacterium tumefaciens"
                                /strain="plasmid pTiA6"
                                /db_xref="taxon:358"
                                /note="TATA-box"
            promoter          60..66
                                /note="polyadenylation signal"
            misc_feature      68..613
                                /note="unidentified reading frame"
            CDS                109..489
                                /codon_start=1
                                /transl_table=11
                                /protein_id="CAA25129.1"
                                /db_xref="GI:39151"
                                /db_xref="SWISS-PROT:P03867"
                                /translation="MNFADTPTLASLDLDWACEEFIKTYGASPOLETGEVQTNNGLLY
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                                PEKGFRLCHNRPFPLYPIVAHGSMS"
            misc_feature      659..664
                                /note="polyadenylation signal"
BASE COUNT  288 a   189 c   139 g   262 t
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Query Match      100.0%; Score 20; DB 1; Length 878;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
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DB 545 CTACGGCAATGTACCAGCTG 564

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RESULT 8
LOCUS      A10942      1037 bp      DNA      PAT      27-SEP-1993
DEFINITION Nucleotide sequence 4 from patent number DE3920034.
ACCESSION  A10942
VERSION     A10942.1 GI:492369
KEYWORDS   .
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 1037)
AUTHORS     .
JOURNAL     .
FEATURES    .
            source
            Location/Qualifiers
                Patent: DE 3920034-A 4 31-MAY-1990;
                /organism="unidentified"
                /db_xref="taxon:32644"
                1..1037
BASE COUNT  338 a 174 c 166 g 359 t
ORIGIN
            1 ctacggcaatgtaccagctg 20
            |||||
Db 841 CTACGGCAATGTACCAGCTG 860

Query Match      100.0%; Score 20; DB 6; Length 1037;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
    |||||
Db 841 CTACGGCAATGTACCAGCTG 860

RESULT 9
LOCUS      A10939      1085 bp      DNA      PAT      27-SEP-1993
DEFINITION Nucleotide sequence 1 from patent number DE3920034.
ACCESSION  A10939
VERSION     A10939.1 GI:492367
KEYWORDS   .
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 1085)
AUTHORS     .
JOURNAL     .
FEATURES    .
            source
            Location/Qualifiers
                Patent: DE 3920034-A 1 31-MAY-1990;
                /organism="unidentified"
                /db_xref="taxon:32644"
                1..1085
BASE COUNT  369 a 218 c 155 g 343 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 1085;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
    |||||
Db 889 CTACGGCAATGTACCAGCTG 908

RESULT 10
LOCUS      A10943      1160 bp      DNA      PAT      27-SEP-1993
DEFINITION Nucleotide sequence 5 from patent number DE3920034.
ACCESSION  A10943
VERSION     A10943.1 GI:492370
KEYWORDS   .
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 1160)
AUTHORS     .
JOURNAL     .
FEATURES    .
            source
            Location/Qualifiers
                Patent: DE 3920034-A 5 31-MAY-1990;
                /organism="unidentified"
                /db_xref="taxon:32644"
                1..1160
BASE COUNT  367 a 194 c 188 g 411 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 1160;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
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Db 964 CTACGGCAATGTACCAGCTG 983

RESULT 11
LOCUS      A10941      1166 bp      DNA      PAT      27-SEP-1993
DEFINITION Nucleotide sequence 3 from patent number DE3920034.
ACCESSION  A10941
VERSION     A10941.1 GI:492368
KEYWORDS   .
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 1166)
AUTHORS     .
JOURNAL     .
FEATURES    .
            source
            Location/Qualifiers
                Patent: DE 3920034-A 3 31-MAY-1990;
                /organism="unidentified"
                /db_xref="taxon:32644"
                1..1166
BASE COUNT  381 a 208 c 196 g 381 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 1166;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
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Db 1070 CTACGGCAATGTACCAGCTG 1089

RESULT 12
LOCUS      A18051      1186 bp      DNA      PAT      26-JUL-1994
DEFINITION DNA used as a probe for neo gene seq ID No:2.
ACCESSION  A18051
VERSION     A18051.1 GI:583120
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE   1 (bases 1 to 1186)
AUTHORS     .
JOURNAL     .
FEATURES    .
            source
            Location/Qualifiers
                Patent: WO 9209696-A 2 11-JUN-1992;
                /organism="synthetic construct"
                /db_xref="taxon:32630"
                1..1186
            promoter
            /note="sequence derived from tapetum specific promoter of
            Nicotiana tabacum"
            167..790
            gene
            /gene="neomycine phosphotransferase gene"
            167..790
            CDS
            /gene="neomycine phosphotransferase gene"
            /note="Protein sequence is in conflict with the conceptual
            translation"

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/codon_start=1
/transl_table=11
/db_xref="GI:4529900"
/transl_table="NEIQDRAARLSWATGVCFAAALDVVTAGRDWLLGLGEVPGQD
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EEHQGLAPAEKVLARLARPMDGDGLVTHGDACLPNIMVNGRFSGFIDGRLGVADR
YQDIALATRDIAELGEGWADRFVLVIGINAPDSQRIAFYRLDDEF"
polyA_site
1055..1186
/note="3', regulatory sequence containing the
polyadenylation site derived from agrobacterium T-DNA gene
7"

BASE COUNT      244 a   317 c   325 g   300 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 1186;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
|||||
Db 1033 CTACGGCAATGTACCAGCTG 1052

RESULT 13
AR095107
LOCUS      AR095107      1186 bp      DNA      PAT      08-SEP-2000
DEFINITION Sequence 2 from patent US 6002070.
ACCESSION AR095107
VERSION AR095107.1 GI:10022665
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1186)
AUTHORS D'Halluin,K. and Gobel,E.
TITLE Process for transforming monocotyledonous plants
JOURNAL Patent: US 6002070-A 2 14-DEC-1999;
FEATURES
source 1..1186
/organism="unknown"
BASE COUNT      244 a   317 c   325 g   300 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 1186;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
|||||
Db 1033 CTACGGCAATGTACCAGCTG 1052

RESULT 14
AR098313
LOCUS      AR098313      1186 bp      DNA      PAT      14-FEB-2001
DEFINITION Sequence 2 from patent US 6074877.
ACCESSION AR098313
VERSION AR098313.1 GI:12807570
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1186)
AUTHORS D'Halluin,K. and Gobel,E.
TITLE Process for transforming monocotyledonous plants
JOURNAL Patent: US 6074877-A 2 13-JUN-2000;
FEATURES
source 1..1186
/organism="unknown"
BASE COUNT      244 a   317 c   325 g   300 t
ORIGIN
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ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 1186;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
|||||
Db 1033 CTACGGCAATGTACCAGCTG 1052

RESULT 15
AX012338
LOCUS      AX012338      1186 bp      DNA      PAT      06-SEP-2000
DEFINITION Sequence 2 from Patent EP0955371.
ACCESSION AX012338
VERSION AX012338.1 GI:9998387
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1186)
AUTHORS D'Halluin,K. and Gobel,E.D.
TITLE Process for transforming monocotyledonous plants
JOURNAL Patent: EP 0955371-A 2 10-NOV-1999;
FEATURES
source 1..1186
/organism="synthetic construct"
misc_feature 1..8
/note="DNA used as probe for neo gene"
misc_feature 9..790
/note="sequence derived from tapetum specific promoter of
Nicotiana tabacum"
misc_feature 791..1186
/note="coding sequence of neomycine phosphotransferase"
/note="3', regulatory sequence containing the
polyadenylation site derived from Agrobacterium T-DNA gene
7"
BASE COUNT      244 a   317 c   325 g   300 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 1186;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
|||||
Db 1033 CTACGGCAATGTACCAGCTG 1052

Search completed: December 19, 2001, 17:27:49
Job time: 3911 sec
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; FEATURE:
; NAME/KEY: -
; LOCATION: 1..8
; OTHER INFORMATION: /note= "sequence derived from
; OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
; FEATURE:
; NAME/KEY: -
; LOCATION: 9..790
; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycine
; OTHER INFORMATION: phosphotransferase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: 791..1186
; OTHER INFORMATION: /label= 3'g7
; OTHER INFORMATION: /note= "3', regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA gene 7"
US-08-064-121-2

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Query Match 100.0%; Score 20; DB 1; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ctacggcaatgtaccagctg 20
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Db 1033 CTACGGCAATGTACCAGCTG 1052

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RESULT 2
US-08-478-015-2
; Sequence 2, Application US/08478015
; Patent No. 5712135
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,015
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1186 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: probe
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..8
; OTHER INFORMATION: /note= "sequence derived from
; OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
; FEATURE:
; NAME/KEY: -
; LOCATION: 9..790
; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycine phosphotransferase ge
; FEATURE:
; NAME/KEY: -
; LOCATION: 791..1186
; OTHER INFORMATION: /label= 3'g7
; OTHER INFORMATION: /note= "3', regulatory sequence containing the polyadenylat
; OTHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"
US-08-478-015-2

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Query Match 100.0%; Score 20; DB 1; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ctacggcaatgtaccagctg 20
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Db 1033 CTACGGCAATGTACCAGCTG 1052

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RESULT 3
US-08-475-975-2
; Sequence 2, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,975
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:

```

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/ NAME: Crane-Feury, Sharon E
/ REGISTRATION NUMBER: 36,113
/ REFERENCE/DOCKET NUMBER: 010830-043
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1186 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: probe
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 9..790
/ OTHER INFORMATION: /label= NPTII
/ OTHER INFORMATION: /note= "coding sequence of neomycine
/ OTHER INFORMATION: phosphotransferase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 791..1186
/ OTHER INFORMATION: /label= 3'g7
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA gene 7"
/ US-08-475-975-2

Query Match 100.0%; Score 20; DB 3; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
DB 1033 CTACGGCAATGTACCAGCTG 1052

RESULT 4
US-09-084-889-2
/ Sequence 2, Application US/09084889
/ Patent No. 6074877
/ GENERAL INFORMATION:
/ APPLICANT: D'HALLUIN, Kathleen
/ APPLICANT: GOBEL, Elke
/ TITLE OF INVENTION: PROCESS FOR TRANSFORMING
/ TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: George Mason Bldg., Washington & Prince Sts.
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/084,889
/ FILING DATE:
/ CLASSIFICATION:
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/064,121
/ FILING DATE:
/ PRIOR APPLICATION DATA: EP 91401888.2
/ APPLICATION NUMBER:
/ FILING DATE: 08-JUL-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Crane-Feury, Sharon E
/ REGISTRATION NUMBER: 36,113
/ REFERENCE/DOCKET NUMBER: 010830-043
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-8620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1186 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: probe
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..8
/ OTHER INFORMATION: /note= "sequence derived from
/ OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 9..790
/ OTHER INFORMATION: /label= NPTII
/ OTHER INFORMATION: /note= "coding sequence of neomycine
/ OTHER INFORMATION: phosphotransferase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 791..1186
/ OTHER INFORMATION: /label= 3'g7
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA gene 7"
/ US-09-084-889-2

Query Match 100.0%; Score 20; DB 3; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
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DB 1033 CTACGGCAATGTACCAGCTG 1052

RESULT 5
US-08-894-440-2
/ Sequence 2, Application US/08894440
/ Patent No. 6025546
/ GENERAL INFORMATION:
/ APPLICANT: PLANT GENETIC SYSTEMS N.V.
/ TITLE OF INVENTION: Method to obtain male sterile plants
/ FILE REFERENCE: NMSCOR
/ CURRENT APPLICATION NUMBER: US/08/894,440
/ CURRENT FILING DATE: 1997-11-12
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 1303
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HindIII-EcoRI
/ OTHER INFORMATION: fragment of pTS88
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (36)..(694)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (695)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1288)..(1303)
OTHER INFORMATION: polylinker of pGEM2
US-08-894-440-2

Query Match      100.0%; Score 20; DB 3; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ctacggcaatgtaccagctg 20
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Db 1098 ctacggcaatgtaccagctg 1117

RESULT 6
US-09-080-625-3
; Sequence 3, Application US/09080625
; Patent No. 6307123
; GENERAL INFORMATION:
; APPLICANT: Kriz, Alan L.
; APPLICANT: Spencer, T. Michael
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
; TITLE OF INVENTION: IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080.625
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Robert E.
; REGISTRATION NUMBER: P-42,628
; REFERENCE/DOCKET NUMBER: DEKM.161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3153 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; TOPOLOGY: linear
US-09-080-625-3

Query Match      100.0%; Score 20; DB 4; Length 3153;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ctacggcaatgtaccagctg 20
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Db 2679 CTACGGCAATGTACCAGCTG 2698

RESULT 7
US-08-453-104-23
; Sequence 23, Application US/08453104
; Patent No. 5633446
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; TITLE OF INVENTION: IN PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453.104
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
US-08-453-104-23

Query Match      100.0%; Score 20; DB 1; Length 3200;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ctacggcaatgtaccagctg 20
| | | | | | | | | | | | | | | | | |
Db 2952 CTACGGCAATGTACCAGCTG 2971

RESULT 8
US-08-694-824-23
; Sequence 23, Application US/08694824
; Patent No. 5877306
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; TITLE OF INVENTION: IN PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,824
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
US-08-694-824-23

Query Match 100.0%; Score 20; DB 2; Length 3200;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1 ctacggcaatgtaccagctg 20
| | | | | | | | | | | | | | | | | |
Db 2952 CTACGGCAATGTACCAGCTG 2971

RESULT 9
US-08-453-104-22
; Sequence 22, Application US/08453104

; Patent No. 5633446
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; TITLE OF INVENTION: IN PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,104
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2151..2155
; OTHER INFORMATION: /note= "Nucleotides 2151-2155
; OTHER INFORMATION: wherein N is not known."
US-08-453-104-22

Query Match 100.0%; Score 20; DB 1; Length 3201;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 ctacggcaatgtaccagctg 20
| | | | | | | | | | | | | | | | | |
Db 3025 CTACGGCAATGTACCAGCTG 3044

RESULT 10
US-08-694-824-22
; Sequence 22, Application US/08694824
; Patent No. 5877306
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

```
;; TITLE OF INVENTION: IN PLANT CELLS
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: George Mason Bldg., Washington & Prince Sts.
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/694,824
;; FILING DATE: 09-AUG-1996
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/937,869
;; FILING DATE: 16-DEC-1992
;; APPLICATION NUMBER: GB 90401055.0
;; FILING DATE: 18-APR-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rea, Teresa S
;; REGISTRATION NUMBER: 30,427
;; REFERENCE/DOCKET NUMBER: 010830-032
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3201 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: 2151..2155
;; OTHER INFORMATION: /note="Nucleotides 2151-2155
;; where N is not known."
US-08-694-824-22
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Query Match 100.0%; Score 20; DB 2; Length 3201;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ctacggcaatgtaccagctg 20
|||||
Db 3025 CTACGGCAATGTACCAGCTG 3044
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RESULT 11
US-09-080-625-2
; Sequence 2, Application US/09080625
; Patent No. 6307123
; GENERAL INFORMATION:
; APPLICANT: Kriz, Alan L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
; IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,625
; FILING DATE:
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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Robert E.
; REGISTRATION NUMBER: P-42,628
; REFERENCE/DOCKET NUMBER: DEKM:161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-080-625-2
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```
Query Match 100.0%; Score 20; DB 4; Length 3336;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ctacggcaatgtaccagctg 20
|||||
Db 2862 CTACGGCAATGTACCAGCTG 2881
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RESULT 12
US-09-080-625-5
; Sequence 5, Application US/09080625
; Patent No. 6307123
; GENERAL INFORMATION:
; APPLICANT: Kriz, Alan L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
; IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,625
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Robert E.
; REGISTRATION NUMBER: P-42,628
; REFERENCE/DOCKET NUMBER: DEKM:161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-080-625-5
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; EARLIER FILING DATE: 1996-07-31

EARLIER FILING DATE: 1996-07-31

; EARLIER

; EARLIER APPLICATION NUMBER: PCT/EP

; EARLIER APPLICATION NUMBER: PCT/EP96/03366

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;; EARLIER FILING DATE: 1996-07-31
;; EARLIER APPLICATION NUMBER: EP 95401844.6
;; EARLIER FILING DATE: 1995-08-04
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 5560
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
;; OTHER INFORMATION: plasmid pTHW142
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(25)
;; OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from
;; OTHER INFORMATION: pTiB6S3
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (84)..(296)
;; OTHER INFORMATION: 3' g7: 3' untranslated region containing the
;; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
;; OTHER INFORMATION: T-DNA
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (318)..(869)
;; OTHER INFORMATION: Bar: region coding for phosphinotricin
;; OTHER INFORMATION: acetyltransferase
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (830)..(2760)
;; OTHER INFORMATION: PSSU: promoter region of Rubisco small subunit
;; OTHER INFORMATION: gene of Arabidopsis thaliana
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (2765)..(3058)
;; OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
;; OTHER INFORMATION: containing polyadenylation signals
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (3059)..(5056)
;; OTHER INFORMATION: uidA: region coding for beta-glucuronidase
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (4483)..(4671)
;; OTHER INFORMATION: IV2: region corresponding to the second intron of
;; OTHER INFORMATION: the St-LS1 gene
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5067)..(5502)
;; OTHER INFORMATION: P35S: 35S promoter region of CaMV
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5533)..(5560)
;; OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
;; OTHER INFORMATION: pTiB6S3
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5058)..(5059)
;; OTHER INFORMATION: region with unknown sequence (may contain up to 20
;; OTHER INFORMATION: nucleotides)
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5077)..(5078)
;; OTHER INFORMATION: region with unknown sequence (may contain up to 20
;; OTHER INFORMATION: nucleotides)
;; FEATURE:
;; NAME/KEY: misc_feature
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;; OTHER INFORMATION: region with unknown sequence (may contain up to 20
;; OTHER INFORMATION: nucleotides)
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US-08-817-188-5

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Query Match      100.0%; Score 20; DB 3; Length 5560;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
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Db 230 CTACGGCAATGTACCAGCTG 211
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Job time: 4274 sec

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